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(54) Title: METHODS AND COMPOSITIONS FOR ALTERING PHYSICAL CHARACTERISTICS OF FRUIT AND FRUIT PRODUCTS

(57) Abstract

Novel plants and methods for their preparation are provided which produce sucrase, particularly heterologous sucrase. The plants may have an increase in the soluble solids content of plant cells, particularly fruit cells as a result. DNA sequences encoding carbohydrate polymer synthesizing enzymes are identified, isolated and inserted into an expression cassette which may then be transformed into plant cells. The method finds particular use in conjunction with fruit-specific transcription for increasing production of carbohydrate polymers in fruit, particularly the apoplast.

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5 **METHODS AND COMPOSITIONS FOR ALTERING PHYSICAL
CHARACTERISTICS OF FRUIT AND FRUIT PRODUCTS**

10 **CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a continuation-in-part of U.S. application Serial No. 265,586 filed November 1, 15 1988, which is a continuation-in-part of U.S. application Serial No. 262,442, filed October 25, 1988, which is a continuation-in-part of U.S. application 20 Serial No. 209,430, filed June 21, 1988, which applications are hereby incorporated herein by reference.

25 **INTRODUCTION**

Technical Field

30 This invention relates to the use of carbohydrate polymers to alter the physical characteristics of fruit and fruit products.

Background

35 Of significant interest to the fruit-processing industry are the physical characteristics of fruit such as the soluble solids composition of ripe fruit. Soluble solids affect storage, handling, commercial processing and cooking of the fruit. Of particular interest is optimization of soluble solids characteristics of succulent fruit with regard to properties such as consistency and/or viscosity.

In various applications, fruit having increased soluble solids, increased or decreased viscosity, or increased or decreased consistency, is desired. Increased soluble solids may be a function of "sink strength," the ability of the plant to translocate carbon to the fruit. Increased fruit sink

activity is especially useful in fruit where high soluble solids content is desirable, such as tomatoes for processing into tomato-based products. Other important fruit characteristics include properties

5 which relate generally to the cohesiveness of a homogeneous mixture of the fruit and the viscosity of the serum which remains after the pulp is removed through centrifugation.

Any modifications to fruit soluble solids,
10 should not however have adverse effects on other desirable qualities or development of the plant or fruit. This includes consideration of the physiological consequences of the soluble solid, such as effects of osmotic potential, and/or any subsequent by-
15 products on the plant, fruit and/or end-user, particularly, when the fruit is used for food. It is especially desirable that methods and compositions are developed to modify soluble solids which are safe for human consumption.

20 It is therefore of interest to obtain fruit having an altered carbohydrate content which may thus result in modified characteristics of the fruit or fruit products. In particular, methods and compositions for transforming a plant to produce fruit
25 having modified solids characteristic are desirable. Furthermore, it is desirable not only to transform the plant cell, but also to obtain the altered carbohydrate composition at a particular stage in the growth of the plant, particularly fruiting. In addition, it is
30 desirable that modification occur not only in a particular tissue, such as fruit, but also in a particular compartment of that tissue, such as the apoplast. It is therefore important to be able to express the carbohydrate polymer of interest using DNA
35 sequences which provide for the desired regulation of expression in the plant host.

Relevant Literature

cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson *et al.*, Mol. Gen. Genet. (1985) 200:356-361; Slater *et al.*, Plant Mol. Biol. (1985) 5:137-147). The studies have focused primarily on mRNAs which accumulate during fruit ripening. One of the proteins encoded by the ripening-specific cDNAs has been identified as polygalacturonase (Slater *et al.*, Plant Mol. Biol. (1985) 5:137-147). A cDNA clone which encodes tomato polygalacturonase has been sequenced. Grierson *et al.*, Nucleic Acids Research (1986) 14:8395-8603. The concentration of polygalacturonase mRNA increases 2000-fold between the immature-green and red-ripe stages of fruit development. This suggests that expression of the enzyme is regulated by the specific mRNA concentration which in turn is regulated by an increase in transcription. DellaPenna *et al.*, Proc. Natl. Acad. Sci. USA (1986) 83:6420-6424. In *vitro* synthesis and processing of tomato fruit polygalacturanase has been described. DellaPenna *et al.*, Plant Physiol. (1988) 86:1057-1063. Mature plastid mRNA for psbA (one of the components of photosystem II) reaches its highest level late in fruit development, whereas after the onset of ripening, plastid mRNAs for other components of photosystem I and II decline to nondetectable levels in chromoplasts. Piechulla *et al.*, Plant Mol. Biol. (1986) 7:367-376.

30

SUMMARY OF THE INVENTION

Novel compositions and methods are provided for modifying the soluble solids composition and physical characteristics of fruit and fruit products. The compositions include a novel DNA sequence encoding Leuconostoc mesenteroides. The methods involve transforming a plant cell of interest with an expression cassette functional in a plant cell comprising a trans-

criptional and translational initiation regulatory region, joined in reading frame 5' to a DNA sequence encoding an enzyme capable of polymerizing a carbohydrate comprising at least one hexose moiety to 5 form a carbohydrate polymer and translational and transcriptional termination regions. To provide for transport of the enzyme to a specific cellular compartment, a DNA sequence encoding a transit peptide may be included in the expression cassette. Expression 10 of the enzyme provides for an increase in the soluble solids composition of the fruit as a result of increased production of carbohydrate polymer. Of particular interest is the replacement of fruit soluble solids such as sucrose with carbohydrate polymers such 15 as dextran or levan, depending upon the desired properties of the fruit or fruit products. Increased concentration of carbohydrate polymer in fruit can be used to alter not only the soluble solids composition of the fruit, but also characteristics, for example 20 viscosity, of fruit products.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the integration of dextran-sucrase in tomato fruit metabolism.

25 Figure 2 shows restriction maps of dextran-sucrase (DS) clones pCGN1222, pCGN1223 and SALI partial digests of pCGN1222 (-16, -18, -1, and -69). pCGN1222-12 is a BamHI deletion of pCGN1222. Each plasmid was transformed into E. coli DH1 and extracts 30 were assayed for DS activity (activity = cpm 14C-glucose incorporated into dextran): S = Sall; P = PstI; X = XbaI; E = EcoRI; B = BamHI; K = KpnI.

Figure 3 shows the restriction map of L. mesenteroides dextran-sucrase gene clone in the λ-fix vector (ds-18) and its derivatives in pUC19. Arrows 35 indicate the direction of the lacZ promoter. The expression of dextran-sucrase activity of each clone in

E. coli is also shown. B, BamHI; E, EcoRI; H, HindIII; K, KpnI; P, PstI; R, EcoRV; S, SalI; Sc, SacI; Sp, SphI; X, XbaI.

Figure 4 shows the nucleotide sequence and flanking regions of the dextranucrase gene from L. mesenteroides. Numbering begins at the 5' end of the sequence. The deduced amino acids are those matching the four peptide sequence and the boxed amino acids are those matching the four peptide sequences deduced from amino acid sequence analysis. An arrow designates the proposed cleavage site for signal sequence removal. Putative promoter and ribosome binding site sequences are underlined. Inverted repeated sequences are underlined with broken arrows.

Figure 5 shows the amino acid analysis profile of the dextranucrase protein. Plotted is an average of three analyses. Cys and Trp percentages could not be determined under HCl cleavage conditions. Error bars indicate standard deviation. Protein sequence matches located within the translated DNA sequences are underlined.

Figure 6 shows a map of the 2A11 genomic clone. The transcriptional start site, the polyadenylation site, the start (ATG) and stop (TGA) sites and the position of the intron are indicated. The hatched region indicates the portion of the genomic clone that was used to make the tagged 2A11 constructions. The bottom portion shows the regions used to construct the 2A11 cassettes including the synthetic oligonucleotide used to insert restriction sites and reconstruct the 3' end.

Figure 7 shows the 2A11 cassette pCGN1241 containing the ampicillin resistance gene.

Figure 8 shows a strategy for construction of a PCR-generated dextranucrase construct.

Figure 9 shows a strategy of construction of 35S/dextranucrase and 2A11 dextranucrase binary

vectors.

Figure 10 shows a strategy for construction of a full length dextran sucrase construct.

5 Figure 11 shows a strategy for cloning PG leader in front of a dextran sucrase gene.

Figure 12 is a Northern analysis of leaves from plants transformed with B. subtilis levansucrase (LVS) gene.

10 (A) Two transformants (4-2, 8-2) contain transcripts that hybridize to the LVS probe, however only one transformant (8-2) is producing a full-length transcript (~2 kb).

(B) mas 5'-LVS-mas 3' construct in pCGN1205.

15

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

In accordance with the subject invention, novel DNA sequences, DNA constructs, methods and compositions are provided which permit modification of 20 the soluble solids composition of fruit by means of an increased synthesis of carbohydrate polymer from carbohydrates such as sucrose which comprise at least one hexose moiety. Plant cells are transformed with an expression cassette comprising a DNA sequence encoding 25 a enzyme such as a sucrase capable of polymerizing a carbohydrate such as sucrose to form a carbohydrate polymer. Timing of expression and/or tissue specificity, may be provided by the use of transcriptional regulatory regions having the desired 30 expression specificity. The DNA sequence may also include a DNA sequence encoding a transit peptide recognized by the plant host to provide for targeting to a specific compartment within a tissue of interest, such as fruit apoplast.

35 Modification of the soluble solids composition of a fruit offers potential means to alter specific properties of the fruit. By "modification of the

soluble solids composition of fruit" is intended the replacement of sucrose, glucose and fructose or other soluble sugars with carbohydrate polymers. Of special interest are carbohydrate polymers which are not readily degraded. Although degradation of the polymer may be useful to achieve desired properties in some instances, most preferred is an investment in solids which will not be withdrawn later by degradation or other means. A related concern is the potential for an undesired accumulation of hexose monomers which may cause stress to the cell. Thus, polymers which are "unfamiliar" carbohydrate polymers, i.e., polymers which are not naturally found in the particular plant host of interest, may have special use because the plant is unlikely to possess an enzyme capable of degrading the unfamiliar polymer.

In addition to the effects of a modified carbohydrate profile from replacement of sucrose carbons with carbohydrate polymer carbons, the soluble solids of the fruit may be increased by the stimulation of added carbon flow to the fruit. If the draw of sucrose to carbohydrate polymer strengthens carbon-sink activity in the fruit, a corresponding increase in soluble solids may be achieved.

Considerations for use of a specific sucrase in fruit for the conversion of sucrose to a carbohydrate polymer include pH optimum of the enzyme, the availability of substrate and co-factors required by the enzyme. The sucrase enzyme of interest should have kinetic parameters compatible with the biochemical found in the host plant cell. For example, sucrase may have to compete for substrate with other enzymes, such as invertase. Analysis of the K_m and specific activity of the enzymes in question should be considered in determining the suitability of a sucrase for polymer production in a given host plant. Furthermore, in some cases, it may be desirable to target the enzyme to a

specific location. For example, in tomato it is desired to target the sucrase to the apoplast. The enzyme would thus need to be one which can function under conditions present in the apoplast.

5 For purposes of this invention, it is preferable to replace the native soluble solids with carbohydrate polymers which have, for example, different viscosity and/or consistency coefficients from the soluble solids of the fruit host. Replacement
10 of tomato solids with levan, a viscous carbohydrate in pure solution, reduces gross viscosity and serum viscosity of tomato paste under simulated processing conditions. Replacement of tomato solids with dextran increases the gross viscosity of tomato paste. Thus
15 the use of levansucrase and dextransucrase constructs, respectively, are of particular interest.

To provide for an increased expression of sucrase in a plant, a plant cell is transformed with an expression cassette which includes in the 5'-3' direction of transcription, a transcriptional and translational initiation region functional in a plant cell; a structural gene encoding a sucrase, preferably including a sequence encoding a transit peptide in reading frame at the 5'-terminus, where the transit
25 peptide directs transfer of the sucrase to the apoplast; and a transcriptional and translational termination regulatory region. By sucrase is intended an enzyme capable of converting sucrose to a carbohydrate polymer. The initiation and termination
30 regulatory regions are functional in the host plant cell and may be either homologous or heterologous to the host plant.

The sucrase gene may be derived from prokaryotic sources, for example, genes for dextransucrase, and
35 other glycosyltransferases, which polymerize the glucose moiety of sucrose to form dextran, may be obtained from various species of Leuconostoc and

Streptococcus, including the soil bacterium L. mesenteroides. Genes for levansucrase, which catalyzes the conversion of sucrose to levan, a fructose polymer and free glucose, may be obtained from a variety of species of bacteria, for example, Aerobacter levanicum, Streptococcus salivarius and Bacillus subtilis.

Preferentially the dextranase gene is derived from Leuconostoc mesenteroides and the levansucrase is derived from Bacillus subtilis. The DNA sequence encoding L. mesenteroides dextranase is provided.

Dextranase derived from L. mesenteroides strain B-512F catalyzes the polymerization of branched dextran (95% α 1->6 linkage and 5%-1->3 branched linkages) from sucrose. In contrast to Streptococcus strains, which typically produce several distinct glucosyltransferases, L. Mesenteroides B-512F produces only one glycosyltransferase, and at high levels. Comparison of the deduced amino acid sequence of dextranase with other sequenced proteins (data base) revealed partial homologies with two other glucosyltransferase proteins: gtfB from S. sobrinus (41.5%) and gtfB from S. mutans (41.7%).

Eukaryotic sources, including plant sources, such as Jerusalem artichoke and some grasses, may also find application. Examples of plant enzymes which also may be used include those involved in the synthesis of fructans from sucrose from a variety of sources (see, for example, Bhatia *et al.*, Phytochem. (1979) 18:923-927; Edelman *et al.*, New Phytol. (1968) 67:517-553; Henby *et al.*, Phytochem. (1980) 19:1017-1020; Satyanarayana, Ind. J. Biochem. Biophys. (1976) 13:261-266; Shiomi, Agric. Biol. Chem. (1980) 44:603-614; Shiomi, Carbohydrate Research (1981) 96:281-292; Shiomi, Carbohydrate Research (1982) 99:157-169; and Singh, Phytochem. (1971) 10:2037-2039).

The structural gene for the sucrase may be obtained in a variety of ways. The gene may be synthesized in whole or in part, particularly where it is desirable to provide plant preferred codons. Thus, all 5 or a portion of the open reading frame may be synthesized using codons preferred by the plant host. Plant preferred codons may be determined from the codons of highest frequency in the proteins expressed in the largest amount in the particular plant species of 10 interest.

Methods for synthesizing sequences and bringing the sequences together are well established in the literature. Where a portion of the open reading frame is synthesized, and a portion is derived from natural 15 sources, the synthesized portion may serve as a bridge between two naturally occurring portions, or may provide a 3'-terminus or a 5'-terminus. Particularly where the signal sequence and the open reading frame encoding the sucrase are derived from different genes, 20 synthetic adapters commonly will be employed. In other instances, polylinkers may be employed, where the various fragments may be inserted at different restriction sites or substituted for a sequence in the polylinker.

The sucrase structural gene may be derived 25 from cDNA, from chromosomal DNA or may be synthesized in whole or in part. For the most part, some or all of the sucrase structural gene will be from a natural source or genes substantially homologous to such sequences. In some situations it may be desirable to 30 modify all or a portion of the codons, for example to enhance expression, by employing host-preferred codons. Methods for identifying sequences of interest have found extensive exemplification in the literature, although in individual situations, different degrees of 35 difficulty may be encountered. Various techniques include the use of probes where genomic or cDNA libraries may be searched for complementary sequen-

ces. Where the structural gene to be inserted is derived from prokaryotic cells, it is desirable to minimize the 3' non-coding region of the prokaryotic gene. The substantial absence of this untranslated region can have a positive effect on the transcription, stability, and/or translation of the mRNA in the plant cells.

When the structural gene is other than a plant gene, in order to have expression of the gene in a plant cell transcriptional and translational initiation regulatory regions functional in a plant cell must be provided. Promoters and translation initiation signals functional in plant cells include those from genes which are present in the plant host or other plant species, for example the ribulose bisphosphate carboxylase small subunit transcriptional initiation region, for example from tobacco; those present in viruses such as the cauliflower mosaic virus (CaMV), for example the 35S transcriptional initiation region; and those associated with T-DNA such as the opine synthase transcriptional initiation regions, for example, octopine, mannopine, agropine, etc. Of particular interest is a transcriptional initiation region in a construct comprising two 35S promoters in tandem; fruit specific promoters, e.g. 2A11 (see co-pending application).

The regulatory regions may be homologous (derived from the original host) or heterologous (derived from a foreign source, or synthetic DNA sequence) to the plant host. In order to join the promoter(s) to the structural gene, the non-coding 5' region upstream from the structural gene may be removed by endonuclease restriction. Alternatively, where a convenient restriction site is present near the 5' terminus of the structural gene, the structural gene may be restricted and an adapter employed for linking the structural gene to a promoter region, where the adaptor provides for lost nucleotides of the structural

gene.

Transport of the sucrase into a particular cellular compartment may be accomplished by the use of a transit peptide to target a cellular compartment of interest, such as the apoplast. The transit peptide is inserted following the promoter sequence(s). The transit peptide and processing signal may be derived from any plant protein which is expressed in the cytoplasm and translocated to the cellular compartment of interest. The transit peptide can be identified by comparing the messenger RNA from the particular polypeptide with the mature product. The amino acid sequence absent from the mature protein and coded for by the messenger beginning at the initiation codon, usually a methionine, will normally be the transit sequence. Fragments from the natural transit sequence which retain their transport activity can also be used. The transit peptide is the sequence capable of directing a peptide joined to the transit peptide to the cellular compartment of interest and may be the whole wild-type transit peptide, a functional fragment thereof, or a functional mutant thereof. The full natural sequence is also included.

For the most part, the transit peptides from one plant are generally recognized by other plants. Thus the transit peptide may be native to or heterologous to the ultimate host in which the chimeric gene comprising the structural gene and transit peptide is introduced. Transit peptides may come from tomato or other fruits or vegetables. The transit peptide will usually have at least about 20 amino acids and not more than about 100 amino acids. Transit peptides of particular interest include leader sequences from genes encoding apoplast proteins produced in the cytoplasm, then translocated to the apoplast. Such proteins

include polygalacturonase (see Sheehy *et al.*, Mol. Gen. Genet. (1987) 208:30-36), a cell wall enzyme implicated in the softening of fruit during ripening.

The termination region may be derived from the
5 3'-region of the gene from which the initiation region was obtained or from a different gene. The termination region may be derived from a plant gene, particularly the tobacco ribulose biphosphate carboxylase small sub-unit termination region; a gene associated with the
10 Ti-plasmid such as the octopine synthase termination region; or the tml termination region.

In developing the expression cassette, the various fragments comprising the regulatory regions and open reading frame may be subjected to different
15 processing conditions, such as ligation, restriction enzyme digestion, resection, in vitro mutagenesis, primer repair, use of linkers and adapters, and the like. Thus, nucleotide transitions, transversions, insertions, deletions, or the like, may be performed on the
20 DNA which is employed in the regulatory regions and/or open reading frame. The expression cassette thus may be wholly or partially derived from natural sources, and either wholly or partially derived from sources homologous to the host cell, or heterologous to the
25 host cell. Furthermore, the various DNA constructs (DNA sequences, vectors, plasmids, expression cassettes) of the invention are isolated and/or purified, or synthesized and thus are not "naturally occurring".

30 During the construction of the expression cassette, the various fragments of the DNA will usually be cloned in an appropriate cloning vector, which allows for amplification of the DNA, modification of the DNA or manipulation by joining or removing of sequences,
35 linkers, or the like. Normally, the vectors will be capable of replication in at least a relatively high copy number in E. coli.

A number of vectors are readily available for cloning, including such vectors as pBR322, pUC series, M13 series, etc. The cloning vector will have one or more markers which provide for selection for transformants. The markers will normally provide for resistance to cytotoxic agents such as antibiotics, heavy metals, toxins, or the like. By appropriate restriction of the vector and cassette, and as appropriate, modification of the ends, by chewing back or filling in overhangs, to provide for blunt ends, by addition of linkers, by tailing, complementary ends can be provided for ligation and joining of the vector to the expression cassette or component thereof.

After each manipulation of the DNA in the development of the cassette, the plasmid will be cloned and isolated and, as required, the particular cassette component analyzed as to its sequence to ensure that the proper sequence has been obtained. Depending upon the nature of the manipulation, the desired sequence may be excised from the plasmid and introduced into a different vector or the plasmid may be restricted and the expression cassette component manipulated, as appropriate. The manner of transformation of E. coli with the various DNA constructs (plasmids and viruses) for cloning is not critical to this invention. Conjugation, transduction, transfection or transformation, for example, calcium chloride or phosphate mediated transformation, may be employed.

Depending upon the manner of introduction of the expression construct into the plant, other DNA sequences may be required. Commonly, the expression cassette will be joined to a replication system functional in prokaryotes, particularly E. coli, so as to allow for cloning of the expression cassette for isolation, sequencing, analysis, and the like. Included with the replication system will usually be one or more markers which may allow for selection in the host, the

markers usually involving biocide resistance, for example antibiotic resistance; heavy metal resistance; toxin resistance; complementation, providing phototrophy to an auxotrophic host; immunity; etc. Where

5 the DNA will be microinjected into the host cell, a marker will usually be desirable which allows for selection of those cells in which the injected DNA has become integrated and functional. Thus, markers will be selected which can be detected in a plant host.

10 Alternatively, one may use agrobacteria as a vector for introducing DNA into a plant cell host. A first host vector is transformed with an extrachromosomal element or plasmid capable of maintenance in said first host, where said extrachromosomal element is characterized as being self-transmissible or capable of mobilization with a second helper extrachromosomal element; being capable of conjugal transfer to agrobacteria; containing predetermined DNA segments comprising foreign nucleic acid sequences, such as foreign DNA, 15 encoding a peptide or other genetic information of interest capable of replication, transcription and usually translation in a host cell; and at least one DNA segment homologous with target DNA in agrobacteria, in said agrobacteria, either chromosomal or extrachromosomal; and optionally a marker for selection.

20 Generally, the extrachromosomal elements comprise a vector having a replicon or replication system having a narrow host range. That is, the extrachromosomal elements are capable of maintenance and replication in a first host which is capable of conjugation with agrobacteria having the target DNA, but the vector is incapable of maintenance in the agrobacteria so that the agrobacteria is rapidly cured. In this way, in the absence of integration of at least a portion of the 25 extrachromosomal composition, the extrachromosomal DNA will be lost in the agrobacteria. Thus, the DNA of the extrachromosomal element is rescued by integration with

a stable genetic element of the agrobacteria.

The replicon may come from a plasmid, virus, or other source which allows for stable maintenance in the first host. The first host will normally be a pro-
5 karyote, particularly E. coli. By employing a vector capable of replication in E. coli and other enteric hosts (narrow range), the vector will not be replicated and maintained in non-enteric Gram negative bacteria.
The extrachromosomal element may therefore be a plasmid
10 or virus (phage) or other DNA, which provides the requisite properties.

The extrachromosomal element may also have a mobilization locus, and be self-transmissible, or capable of conjugal transfer by trans-complementation with
15 a helper plasmid having the necessary genes for transfer, e.g., tra. Conveniently, the extrachromosomal DNA and the helper plasmid will be initially employed in different cells, employing tripartite mating, or a variation thereof, rather than dual mating, so that in
20 vitro introduction of both the extrachromosomal DNA and the helper plasmid into the first host cell prior to conjugal transfer is not required. The helper plasmid will have the necessary function for conjugal mobilizability (transfer), as well as a functioning replication
25 system. Another characteristic is the presence of a DNA sequence in the extrachromosomal element of at least about 50bp which is at least substantially homologous with DNA present in the agrobacteria to provide for efficient integration.

30 The homologous DNA in the agrobacteria which serves as the recombination locus may be chromosomal or extra chromosomal. Of particular interest is the T-DNA region of the Ti plasmid, the region of the Ti plasmid between the left and right borders. The region of
35 homology may include regions encoding proteins, regulatory regions, or non-encoding regions and need not have perfect homology. By having regions of at least

substantial homology with the target DNA on both sides of the sucrase expression cassette and in close proximity to the termini of the cassette DNA, the cassette may be inserted into the target host DNA with 5 a minimum amount of the remaining DNA of the extrachromosomal element. Where it is desired to obtain normal plant cells and plants following transformation, the T-DNA sequences used to provide homology will not include the tumor genes, or the tumor 10 genes will have been rendered inactive using means well known to those skilled in the art.

The region of homology will be of a sufficient size to provide for integration, and generally will be about 3000bp, more usually at least about 1000bp, 15 conveniently 500bp, and may be 100bp or 50bp as to each of the fragments. The region of homology is generally present in two segments flanking the nucleic acid sequence of interest, the total number of bases of the segments generally not exceeding about 2000bp. The two 20 segments generally not exceeding about 2000bp. The two segments may be the same or different, both as to size and sequence, or may be a wild type or mutant T-DNA sequence, interrupted by the intervening sequences; alternatively, one T-DNA sequence will suffice as 25 described by Comai et al., Plasmid (1983) 10:21-30.

The use of T-DNA for transformation of plant cells has received extensive study and is amply described in EPA Serial No. 120,516, Hoekema, In: The Binary Plant Vector System, Offsetdrukkerij Kanters B.V., Albllasserdam, 1985, Chapter V, Knauf, et al., "Genetic Analysis of Host Range Expression by Agrobacterium", In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed., Springer-Verlag, NY, 1983, p. 245, and An et al., EMBO J. (1985) 4:277-284.

35 Conveniently, explants, cotyledons, or other plant tissue may be cultivated with A. tumefaciens or A. rhizogenes to allow for transfer of the expression

construct to the plant cells, the plant cells dispersed in an appropriate selective medium for selection, grown to callus, shoots grown and plantlets regenerated from the callus by growing in rooting medium. The agrobacterium host will contain a plasmid having the vir genes necessary for transfer of the T-DNA to the plant cells and may or may not have T-DNA. If the expression construct is to be inserted into the host cell by injection or electroporation, disarmed Ti-plasmids (lacking the tumor genes, particularly the T-DNA region) may be used.

Various techniques exist for determining whether the desired DNA sequences present in the plant cell are integrated into the genome and are being transcribed. Techniques such as the Northern blot can be employed for detecting messenger RNA which codes for the sucrase. In addition, the presence of expression can be detected in a variety of ways, such as assaying for enzyme activity or immunoassay for the protein product. A desired phenotype in this case is the presence of increased solids as polymers in the plant fruit, especially the presence of dextran or levan.

The cells which have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick et al., Plant Cell Reports (1986) 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, identifying the resulting hybrid having the desired phenotypic characteristic. Two or more generations may be grown to ensure that the subject phenotypic characteristic is stably maintained and inherited and then seeds harvested for use to provide fruits with the new phenotypic property, particularly increased solids due to production of carbohydrate polymers, especially levan and dextran.

Modification of the carbohydrate profile of fruit may be used to alter the characteristics of fruit

products destined for human consumption. Thus, the safety of any food additive is an important consideration. Dextran is used clinically as a blood plasma extender. It formerly had U.S. "G.R.A.S." 5 (generally recognized as safe) status as a food additive, but was dropped from the list solely due to disuse. One mole of glucose or fructose is released by the respective reactions of dextranase and levansucrase for each mole of sucrose consumed. Thus, 10 even massive sucrose conversion should not "starve" the other metabolic needs of the fruit. Since the osmotic potential of one mole of sucrose is relatively equivalent to one mole of glucose or fructose monomer, the plant additionally will not be stressed and yield 15 affected.

The following examples are offered by way of illustration and not by limitation.

20

EXPERIMENTAL

E. Coli 71-1.8; pCGN783 was deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland, 20852, on December 23, 1988 and given Accession No. 67868.

25

Example 1

Effects of Carbohydrate Polymers on Viscosity of Tomato Paste

Effects on Viscosity

30 Polymers in water were added to tomato paste, which was then evaporated to achieve the desired level of total solids for each measurement. In all of these experiments, the polymer replaces part of the tomato solids. As a result, no change in the viscosity of the 35 paste would be expected if the viscosity of the added polymer is equal to the average viscosity of the tomato solids that were replaced.

5 A. Levan

Modeling studies were done with levan from Aerobacter levanicum. This polymer is similar in structure to the levan produced by Streptococcus salivarius. Although levan is very viscous in pure solution, the polymer appears to break down under simulated tomato processing conditions. Thus, levan caused reductions in the gross viscosity and the serum viscosity of the tomato paste (Table 1).

10

15 Table 1

Effect Of Levan On Tomato Paste Viscosity

Hot break tomato juice	<u>Bostwick (cm)</u>	<u>Ostwald (centipoles)</u>	
control		4.5	597
+0.75% levan	5.8	198	

20 Bostwick consistency was measured at 10% total solids. Ostwald viscosity was measured on clear serum from paste at 6% total solids.

25 B. Dextran

Preliminary results from addition of dextran to tomato paste suggested that a dextran obtained from the Leuconostic mesenteroides B-512F increased Ostwald viscosity in both hot break paste and cold break paste (Table 2).

Table 2Effect Of Dextran On
Tomato Paste Viscosity

	Cold break tomato paste	<u>Bostwick (cm)</u>	<u>Ostwald (centipoles)</u>
control	7.5	152	
+0.5% dextran	9.5	297	
	Hot break tomato paste	<u>Bostwick (cm)</u>	<u>Ostwald (centipoles)</u>
control	6.2	271	
+0.5% dextran	6.5	430	

Table 2 (cont'd)

15 Bostwick consistency was measured at 13% total solids (cold break paste) or at 10.8% total solids (hot break paste). Ostwald viscosity was measured on clear serum from paste at 6% solids.

20 C. Inulin
Inulin is a storage polymer produced by a number of higher plants which are grown for human consumption (e.g. Jerusalem artichoke and dandelion).
25 No consistent effect on viscosity was observed when an inulin suspension was added to tomato paste at room temperature. The inulin used did not dissolve completely, however, unless heated to 80°C. Heating the inulin together with the tomato paste provided a more accurate model of how the inulin would be dispersed through the paste during processing. The temperature of the paste was then lowered for viscosity measurements. The result of this treatment was an increase in gross viscosity of the inulin-containing
30 paste (Table 3).
35

Table 3Effect Of Inulin On
Tomato Paste Viscosity

5

(a) Inulin suspension added to cold break tomato paste.

		<u>Bostwick (cm)</u>	<u>Ostwald (centisoles)</u>
10	Trial I control	10.0	83
	+0.5% inulin	8.9	68
15	Trial II control	11.0	71
	+0.5% inulin	12.9	65

(b) Inulin suspension added to hot break tomato paste.

15

		<u>Bostwick (cm)</u>	<u>Ostwald (centisoles)</u>
20	Trial I control	6.0	270
	+0.5% inulin	7.0	271
25	Trial II control	6.5	271
	+0.5% inulin	5.7	225

(c) Inulin heated together with cold break tomato
paste.

25

		<u>Bostwick (cm)</u>	<u>Ostwald centisoles</u>
30	Trial I control	11.0	71
	+0.5% inulin	6.5	79

Dextranase Enzymology

35 Dextranase activity was assayed under conditions chosen to approximate the environment of the tomato fruit apoplast as follows: 10 mM sucrose, 50 mM

glucose, 50 mM fructose, 3 mM CaCl_2 , 50 mM sodium acetate pH 4.2, 0.02% NaN_3 , 0.1 mg/ml Tween 80 and 25°C. (Daman *et al.* Plant Physiol. (1988) 87:731-736) Dextran polymer was isolated by ethanol precipitation, lyophilized and redissolved in 0.02% NaN_3 . Dextran was assayed by the phenol-sulfuric acid method using glucose as the standard. Under these conditions, dextransucrase converted most of the sucrose into dextran polymers. The results were as shown in Table 4. Gel filtration and dextranase digestion demonstrated that the dextran synthesized in vitro had a structure indistinguishable from that of native dextrans. Only small amounts of the acceptor reaction products leucrose and isomaltose were produced. Thus, glucose and fructose were not readily used as acceptors and, at the concentrations found in tomato, they did not prevent the synthesis of high molecular weight dextran polymers.

20

Table 4

Dextransucrase: Reaction in vitro

25

reaction mixture	mg	% yield
complete (14 U/ml enzyme)	18	74
-minus enzyme control	none	0
-boiled enzyme control	none	0
-minus sucrose control	none	0

30

High molecular weight dextran polymer was also produced when dextransucrase and sucrose were added to serum from ripe tomato fruits (Table 5). This indicates that the tomato does not contain significant concentrations of any unknown substances that prevent

dextran sucrase from producing high molecular weight dextran (e.g., inhibitors or acceptors).

5

Table 5Dextran Synthesis in Tomato Fruit Serum¹

	<u>Reaction Mixture</u>	<u>High molecular weight carbohydrate (μg)</u>
10	a ripe fruit serum	0
	b serum+sucrose	74
	c serum+dextran sucrase	40
	d serum+sucrose+dextran sucrase	308
	e reaction mixture d + dextranase	80

15 ¹Sephadryl S-1000 gel filtration chromatography was performed on the reaction mixtures above. High molecular weight carbohydrate which eluted at the void volume had a molecular mass of >100,000 kDa. The 108 μg of high molecular weight carbohydrate in the original serum was substrated from the carbohydrate content of all reaction mixtures. High molecular weight carbohydrate was synthesized when sucrose and dextran sucrase were added together (reaction mixture d). The newly synthesized dextran was hydrolyzed to low molecular weight products by treatment with dextranase enzyme (reaction mixture e).

20 In order to function in the tomato fruit apoplast, dextran sucrase must compete for substrate with invertase (see Figure 1). The K_m for sucrose and the specific activity of these two enzymes were relatively close as shown in Table 6, below.

30

Table 6Integration of Dextran sucrase in Tomato Fruit Metabolism

35

	<u>K_m for sucrose (mM)</u>	<u>Specific activity (units/mg protein)</u>
	Tomato fruit invertase 6	320
	Dextran sucrase 14	170

Thus, dextranase can compete successfully for substrate and dextran polymers can be produced in the engineered fruits. At the other extreme, even massive dextran production should not "starve" the other metabolic needs of the fruit because one mole of fructose is released for every mole of sucrose consumed in dextran production.

10

Example 2Isolation and Characterization
of Dextranase ClonesConstruction of *L. mesenteroides* DNA Library and
Screening for Clones Expressing the Dextranase Gene

A Sau3A/Lambda-Fix (Stratagene) library was constructed, following the procedures supplied by the manufacturer, from *L. mesenteroides* DNA isolated from a late exponential phase culture of *L. mesenteroides* grown in GYC medium at 30°C. GYC medium has the following formulation: 10 g/l potassium phosphate (pH 6.7); 2 g/l yeast extract (Difco); 5 g/l casein hydrolysate (Gibco); 20 g/l glucose; and 5 ml/l salts solution (40 g $MgSO_4 \cdot H_2O$, 2 g NaCl, 2 g $FeSO_4 \cdot 7H_2O$, and 2 g $MnSO_4 \cdot H_2O$ per liter of water). DNA was partially digested with Sau3A to generate a random population of fragments averaging approximately 15-20 kb in size. Lambda-Fix is an EMBL vector modified so that the phage arms cannot ligate to themselves or to the stuffer fragment. In addition, the Sau3A partially-digested DNA is modified so that it cannot form multimers, eliminating the need to size fractionate the insert DNA. Sau3A partially-digested *L. mesenteroides* DNA was ligated into Lambda-Fix and packaged in vitro into viable phage particles. The Sau3A/Lambda-Fix library consists of approximately 100 genomes worth of *L. mesenteroides* DNA consisting of 10^5 plaque-forming units.

Recombinant phage (5×10^3) were screened for dextranase expression by the method of Gilpin et al. (Infect. Immun. (1985) 49:414) by plating with E. coli in Luria top agar (10 g/l tryptone, 5 g/l yeast extract, 10 g/l NaCl, 0.8% agar) over M-9 minimal salts agar (30 g/l 30g/l KH_2PO_4 ; 53g/l Na_2HPO_4 ; 5g/l NaCl; 10g/l NH_4Cl ; 2g/l glucose; 1mM MgSO_4 ; 0.1mM CaCl_2), containing 0.4% sucrose; 0.1mg/ml dextran T-10; 1 μ g/ml thiamine; 8 μ g/ml leucine; 8 μ g/ml threonine, pH 7.5, and incubating at 30°C. The E. coli (strain C600) cannot utilize sucrose as a carbon source, therefore only weak growth of bacteria occurs in the top agar generating very small plaques. When the dextranase gene is present and expressed, dextran is produced and appears as a white halo around the plaque. Growth of E. coli is also stimulated around the plaque, presumably feeding off of the monosaccharides being released as dextrans are formed. Approximately 1% of the phage screened produced white halos of polymer around the plaques.

Dextran-producing plaques were isolated and partially purified. The clones were further analyzed by assaying for the incorporation of ^{14}C into polysaccharide polymer from sucrose labeled specifically in the glucose or fructose moiety. Polymer was picked from each of the putative dextranase clones growing in Luria top agar over sucrose minimal agar as described above and suspended in 100 μ l of DS buffer (200mM NaOAc, pH5.2, 0.1g/l Dextran T-9, 1.0g/l Tween 80, 1.0mM CaCl_2 , 0.04% NaN_3). Half of the suspension (50 μ l) was then transferred to a reaction tube containing 0.1 μ Ci of dried sucrose [glucose- ^{14}C] with 50 μ l DS substrate (DS buffer, 6.8g/l sucrose) and the other half to a reaction tube containing sucrose [fructose- ^{14}C] with 50 μ l DS substrate. The reactions were then incubated at 30°C for approximately 16 hrs. An aliquot of each

reaction (10-30 μ l) was then spotted onto Whatman No.1 filter paper. The filters were washed in three changes of methanol (10ml/filter/change) on a table top shaker for 10 minutes/change, then air dried and counted in 5 5ml scintillation fluid in a Beckman Scintillation Counter. Germaine *et al.*, J. Dent. Res. (1974) 53: 1355-1360. All of the clones incorporated sucrose-derived ^{14}C -fructose and not ^{14}C -glucose into polymer indicating that the clones were expressing 10 levansucrase rather than dextranSucrase. In addition, reactivation of the enzyme produced after SDS-PAGE and PAS staining for carbohydrates (Miller and Robyt, Anal. Biochem. (1986) 156:357-363) revealed a protein with the mobility expected for levansucrase (116 kd).

15 Rescreening of the Lambda-Fix library was performed as described above except that the medium was first buffered to pH 6. The pH optimum of dextran- 20 sucrase is pH 5.2. LB media is approximately pH 7.5 and increases to approximately pH 8 as the E. coli grow. At pH 8, dextranSucrase retains only 10% of maximal activity, but this value is 80% at pH 6.0. Twenty clones producing halos were picked and assayed by the ^{14}C -labeling assay described above. One clone, DS-18, incorporated sucrose derived ^{14}C -glucose and was 25 purified.

Example 3

Analysis of cDNA Clones

Determination of dextranSucrase activity

30 DNA was isolated the DS-18 lambda clone and a partial restriction map was produced. A fragment containing the dextranSucrase gene was subcloned as an XbaI fragment from DS-18 into pUC19 in both orientations (pCGN1222, pCGN1223). The plasmids were used to transform a DNA stabilizing strain of E. coli (DH1, recA). Maniatis *et al.*, Molecular Cloning: A Laboratory Manual (Cold Springs Harbor, 1982).

Extracts were then prepared and assayed for DS activity by the sucrose [glucose-¹⁴C] incorporation assay described above. Only one orientation of the insert (pCGN1222) resulted in expression of DS activity.

5 Plasmids containing SalI partial deletions of pCGN1222 in DH1 were plated on SYC media (same as GYC media except sucrose is substituted for glucose) and grown at 30°C until colonies showed the large viscous colonies characteristics of dextran production at approximately
10 nine days. The clones were further analyzed for DS activity by the sucrose [glucose-¹⁴C] incorporation assay described above. Those colonies producing dextran also incorporated ¹⁴C-glucose while colonies not producing dextran did not incorporate
15 ¹⁴C-glucose. Due to the orientation-dependent expression of DS described above, the 5' end of the DS gene was proposed to be at the left end of the pCGN1222 insert as shown in Figure 2.

Additional information was obtained by
20 deletion of the BamHI fragment from pCGN1222 to form pCGN1222-12 (Fig. 2). The resulting plasmid retained the ability to incorporate ¹⁴C-glucose from sucrose [glucose-¹⁴C], although the activity appeared reduced. The remaining 5' 6.8kb fragment therefore
25 presumably contains the majority of the DS gene, with perhaps some portion of the gene located beyond the BamHI site. Deletions were made to the pCGN1222 derivatives shown in Figure 2 to form the corresponding plasmids shown in Figure 3 using Promega's Erase-a-Base system.
30 Progressive unidirectional deletions were made using exonuclease III which specifically digests DNA from 5' protruding or blunt ends while leaving 4 base 3' protruding ends intact. For example, plasmid pCGN1222-12 was cut with XbaI to generate a 5'
35 protruding end and deletions were made approximately 3kb into the insert. The plasmid was also cut with SphI to generate a 3' protruding end thus protecting

the vector from digestion. Deletions were then transformed into E. coli (DH1), plated onto SYC media, and screened for DS activity by the sucrose [glucose-¹⁴C] incorporation method described above. Plasmid DNA was isolated and restriction mapped from various colonies, both positive and negative for DS activity. The 5' boundary of the DS coding region was determined by comparing the restriction maps and DNA sequences of two clones, of pCGN2023, clones 5-1 and 5-7. Clone 5-1 does not incorporate ¹⁴C-glucose. The 5' end of the insert maps 161bp 5' to the first PstI site and does not contain the first HindIII site. Clone 5-7 does incorporate ¹⁴C-glucose and the 5' end of the insert maps 265bp 5' to the first PstI site and contains the first HindIII site (Fig. 3). Clone 5-1 does not contain the putative ATG initiation codon. Clone 5-7 contains an ATG (Met) codon which begins a 4.78kb open reading frame, and therefore is proposed to be the start site for DS translation. Clone 5-7 represents the shortest active fragment obtained.

DNA Sequencing

The DNA sequence of the dextrantrasucrase (DS) gene was determined by the dideoxy-chain termination method of Sanger et al. (1977) using M13 single-stranded templates or double-stranded DNA (Chen and Seeburg) and the modified bacteriophage T7 polymerase (Sequences) (Tabor and Richardson). Fragments were subcloned into M13mpl8 (Yannich-Perren et al., Gene (1985) 33:103-119) or a bluescribed M13+ chloramphenicol derivative (Stratagene, San Diego, CA) and nested deletions were created using the Erase-a-Base System (Promega Biotec). Synthetic oligonucleotide primers were synthesized on an Applied Biosystems model 380A DNA synthesizer to sequence through gaps and to determine the sequence of the complementary strand. Both strands of the Dex gene were completely sequenced. The sequence data were analyzed using the

IntelliGenetics Suite of molecular programs version S.3. The sequence is shown in Fig. 4.

Physical Characterization of the Gene Product of DS18

5 Purified DS18 plaques were plated (10^4 plaques/plate) onto M-9 sucrose (pH 6) in LB top agar (pH 6) and incubated at 30°C until polymer formation appeared (36-48 hrs). The top agar was scraped off and soaked in DS buffer (200mM NaOAc, pH5.2, 0.1g/l Dextran T-9, 10 1.0g/l Tween 80, 1.0mM CaCl₂, 0.04% NaN₃) to elute any proteins. The agar was then pelleted and the supernatant concentrated to approximately 50 µl. Sample buffer (0.05M Tris-HCl pH 6.8, 1.0% SDS, 5% β -mercaptoethanol, 10% glycerol, 0.005% bromophenol blue) was added and 15 the samples were analyzed by SDS-PAGE. Silver staining revealed a protein band slightly larger than the size expected for dextranase (177 kd).

Comparison of DNA Sequence of DS18 Clone to Protein

20 Sequence of Dextranase

Partially-purified dextranase protein (Miller *et al.*, Carbohydrate Res. (1986) 147:119-133) was carboxymethylated and submitted to SDS-PAGE. A dextranase band was observed at 177 kd and a 25 dextranase breakdown product formed a band at 158 kd. The breakdown product retains enzyme activity.

The majority of the protein preparation was concentrated (through Speed-Vac lyophilization) 10 fold and loaded onto four 0.5 mm 10% Laemmli SDS gels. Dextranase was separated from other contaminants by 30 electrophoresis of gel for 60 min at 200v. The gel was stained for 2-4 min in 0.1% commassie blue, 47% methanol, 47% water, and 6% acetic acid; then destained in 50% methanol for 4-6 min. The clearly visible dextranase band in the upper portion of the gel was 35 excised and soaked in 0.5% SDS, 1mM N-ethylmorpholine, pH 9.0 in preparation for electroelution.

Electroelution was carried out in an ISCO elution device. Gel chips were placed in the chamber assembled with 50kD molecular weight cutoff dialysis tubing and electroeluted for 120 min against 1 mM N-5 ethylmorpholine, pH 9.0 at 4°, 3 watts. Eluted sample was recovered from the concentrating well. The well was rinsed several times with additional buffer and pooled with the eluted sample to make a final volume of 8 ml. Subsequent SDS-PAGE analysis established the 10 presence of a single molecular weight species at approximately 177kD.

Aliquots (5% each) were taken and dried in preparation for amino acid hydrolysis. One sample was performic acid oxidized to enable identification of 15 cysteine and methionine residues. Samples were then subjected to vapor phase HCl/phenol hydrolysis for 24 hr, 110°C in vacuo. Amino acid composition was determined by sample application to a Beckman 6300 amino acid analyzer. (See Figure 5.)

Peptides were generated from one-third of the remaining dextranase to facilitate determination of protein sequence. Chemical cleavage with cyanogen bromide was chosen to optimize the number of peptides generated. The protein was lyophilized to dryness, 20 resuspended in 98% formic acid, then adjusted to 70% formic acid by adding water. β-mercaptoethanol was added to 1%. Cyanogen bromide crystals were added to a concentration of approximately 20-30 mg/ml. The reaction proceeded for 24 hr at room temperature, in 25 the dark at which time a sample was analyzed by SDS gel electrophoresis. The remaining digest was size 30 fractionated over a HPLC TSK 2000sw sizing column in 50% acetonitrile, 0.1% TFA.

Two fractions from this sizing column were 35 each partially dried down and brought up to 100 µl in 0.1% TFA. Further fractionation of the peptides contained in these size cuts was achieved through HPLC

chromatography on a narrow bore, reverse phase C8 column using an acetonitrile/H₂O gradient. Material recovered from this column served as the sample for protein sequencing.

5 Based on a comparison of the readable sequence to the DNA sequence, four peptides were identified in the sequencing sample. The four peptide sequences can be matched to the DNA sequence. The four peptides read as follows:

- 10
- 1) NFGTITAN-A-A-F
 - 2) VDRSNDSTENEAIIPNYSFV-R-D-V
 - 3) D-Y
 - 4) -E/GYAFLEFLQ/VAL

15 (dashes indicate the amino acid at the site was not identified, slashes indicate an either/or situation). The location of the peptide sequences in the translation of the DNA sequence is shown in Figure 5.

20

Example 4
Construction of Levansucrase
Expression Cassette

Plasmid pLS8 containing the B. subtilis levan-

25 sucrase gene was obtained from P. Gay (Gay et al., J. Bacteriol. (1983) 153:1424-1431). The RsaI-EcoRI frag-

ment containing the 5'-end of the gene and the EcoRI-
EcoRV fragment containing the 3'-end of the gene were isolated from polyacrylamide and agarose gels, respec-

30 tively, and ligated into the SmaI site of Bluescribe M13 (minus). The resulting clones, pCGN498 and pCGN499 have the levansucrase gene inserted into the Bluescribe polylinker in opposite directions.

35 Insertion of Levansucrase Gene into the mas Cassette
pCGN1047 is an expression cassette consisting of the 5' and 3' non-coding regions of the mannopine

synthase (mas) gene (position 20804 to 20126) of Barker et al., Plant Mol. Biol. (1983) 2:335-350) with a poly-linker between the 5' and 3' regions. The insert from pCGN499 was excised as a Bam-Sst fragment and ligated 5 into Bam-Sst cut pCGN1047. The resulting plasmid, pCGN1201, contained the levansucrase coding region between the 5' and 3' regions of the mas promoter (Figure 12).

10 Transfer of mas-Levansucrase Construction
into Broad Host Range Binary Plasmid

The binary plasmid used for transfer of the mas-levansucrase construction to Agrobacterium was pCGN783 described in co-pending U.S. application serial number 188,361 filed April 29, 1988 which is hereby 15 incorporated by reference.

(a) Construction of pCGN783

pCGN783 is a binary plasmid containing the 20 left and right T-DNA borders of A. tumefaciens octopine Ti-plasmid pTiA6 (Currier and Nester, J. Bacteriol. (1976) 126:157-165) the gentamicin resistance gene of pPH1J1 (Hirsch et al., Plasmid (1984) 12:139-141), the 35S promoter of cauliflower mosaic virus (CaMV) 25 (Gardner et al., Nucleic Acid Res. (1981) 9:1871-1880); the kanamycin resistance gene of Tn5 (Jorgensen, Mol. Gen. (1979) 177:65); and the 3' region from transcript 7 of pTiA6 (Currier and Nester, supra (1976)).

30 (b) Construction of pCGN587

The HindIII-SmaI fragment of Tn5 containing the entire structural gene for APH3'II (Jorgensen et al., Mol. Gen. (1979) 177:65), was cloned into pUC8 (Vieira and Messing, Gene (1982) 19:259), converting 35 the fragment into a HindIII-EcoRI fragment, since there is an EcoRI site immediately adjacent to the SmaI site. The PstI-EcoRI fragment containing the 3' portion of

the APH3'II gene was then combined with an EcoRI-BamHI-SalI-PstI linker into the EcoRI site of pUC7 (pCGN546W). Since this construct does not confer kanamycin resistance, kanamycin resistance was obtained by inserting 5 the BglI-PstI fragment of the APH3'II gene into the BamHI-PstI site (pCGN546X). This procedure reassembles the APH3'II gene, so that EcoRI sites flank the gene. An ATG codon was upstream from and out of reading frame with the ATG initiation codon of APH3'II. The undesired 10 ATG was avoided by inserting a Sau3A-PstI fragment from the 5' end of APH3'II, which fragment lacks the superfluous ATG, into the BamHI-PstI site of pCGN546W to provide plasmid pCGN550. The EcoRI fragment of pCGN550 containing the APH3'II gene was then cloned 15 into the EcoRI site of pUC8-pUC13 (K. Buckley supra (1985)) to give pCGN551.

Each of the EcoRI fragments containing the APH3'II gene was then cloned into the unique EcoRI site of pCGN451, which contains an octopine synthase cassette for expression to provide pCGN548 (2ATG) and pCGN552 (1ATG). The plasmid pCGN451 having the ocs 5' and the ocs 3' in the proper orientation was digested with EcoRI and the EcoRI fragment from pCGN551 containing the intact kanamycin resistance gene inserted 20 with EcoRI site to provide pCGN552 having the kanamycin resistance gene in the proper orientation. This ocs/KAN gene was used to provide a selectable marker for the 25 trans type binary vector pCGN587.

The 5' portion of the engineered octopine synthase promoter cassette consists of pTiA6 DNA from the XhoI at bp 15208-13644 (Barker et al., supra (1983)), which also contains the T-DNA boundary sequence (border) implicated in T-DNA transfer. In the plasmid pCGN587, the ocs/KAN gene from pCGN552 provides a selectable 30 marker as well as the right border. The left boundary region was first cloned in M13mp9 as a HindIII-SmaI piece (pCGN502) (base pairs 602-2212) and recloned as a

KpnI-EcoRI fragment in pCGN565 to provide pCGN580. As described above, pCGN565 is a cloning vector based on pUC8-Cm, but containing pUC18 linkers. pCGN580 was linearized with BamHI and used to replace the smaller 5 BglII fragment of pVCK102 (Knauf and Nester, Plasmid (1982) 8:45), creating pCGN585. By replacing the smaller SalI fragment of pCGN585 with the XhoI fragment from pCGN552 containing the ocs/KAN gene, pCGN587 was obtained.

10

(c) Construction of pCGN739 (Binary Vector)

To obtain the gentamicin resistance marker, the resistance gene was isolated from a 3.1 kb EcoRI-PstI fragment of pPHIJI (Hirsch et al., Plasmid (1984) 15 12:139-141) and cloned into pUC9 (Vieira et al., Gene (1982) 19:259-268) yielding pCGN549.

The pCGN549 HindIII-BamHI fragment containing the gentamicin resistance gene replaced the HindIII-BglII fragment of pCGN587 creating pCGN594.

20

The pCGN594 HindIII-BamHI region which contains an ocs-kanamycin-ocs fragment was replaced with the HindIII-BamHI polylinker region from pUC18 (Yanisch-Perron, Gene (1985) 33:103-119) to make pCGN739.

25

(d) Construction of 726c (1 ATG-Kanamycin-3' region)

pCGN566 contains the EcoRI-HindIII linker of pUC18 (Yanisch-Perron, ibid) inserted into the EcoRI-HindIII sites of pUC13-Cm (K. Buckley, Ph.D. Thesis, University of California, San Diego, 1985). The HindIII-BglII fragment of pNW31c-8, 29-1 (Thomashow et al., Cell (1980) 19:729) containing ORF1 and 2 (Barker et al., Plant Mol. Biol. (1984) 2:335-350) was subcloned into the HindIII-BamHI sites of pCGN566 producing pCGN703.

30

The Sau3A fragment of pCGN703 containing the 3' region of transcript 7 from pTiA6 (corresponding to bases 2396-2920 of pTl5955 (Barker et al., supra (1984))) was subcloned into the BamHI site of pUC18 (Yanisch-

Perron *et al.*, supra (1985)) producing pCGN709.

The EcoRI-SmaI polylinker region of pCGN709 was replaced with the EcoRI-SmaI fragment from pCGN587 (see 6.1(a), supra) which contains the kanamycin resistance gene (APH3'II) producing pCGN726.

The EcoRI-SalI fragment of pCGN726 plus the BglII-SalI sites of pUC8-pUC13-cm (chloramphenicol resistant, K. Buckley, Ph.D. Thesis, University of California, San Diego, 1985) producing pCGN738. To construct pCGN734, the HindIII-SphI site of Ml3mp19 (Norlander *et al.*, Gene (1983) 26:101-106). Using an oligonucleotide corresponding to bases 3287 to 3300, DNA synthesis was primed from this template. Following S1 nuclease treatment and HindIII digestion, the resulting fragment was cloned into the HindIII-SmaI site of pUC19 (Yanisch-Perron *et al.*, supra (1985)). The resulting EcoRI to HindIII fragment of pTiA6 (corresponding to bases 3390-4494) was cloned into the EcoRI site of pUC8 (Vieira and Messing, supra (1982)) resulting in pCGN734. pCGN726c is derived from pCGN738 by deleting the 900 bp EcoRI-EcoRI fragment.

(e) Construction of pCGN167

pCGN167 is a construct containing a full length CaMV promoter, 1 ATG-kanamycin gene, 3' end and the bacterial Tn903-type kanamycin gene. MI is an EcoRI fragment from pCGN550 (see construction of pCGN587) and was cloned into the EcoRI cloning site in the 1 ATG-kanamycin gene proximal to the polylinker region of Ml3mp9. See copending Application Serial No. 920,574, filed October 17, 1986, which disclosure is incorporated herein by reference.

To construct pCGN167, the AluI fragment of CaMV (bp 7144-7735) (Gardner *et al.*, Nucl. Acids Res. (1981) 9:2871-2888) was obtained by digestion with AluI and cloned into the HincII site of Ml3mp7 (Vieira, Gene (1982) 19:259) to create C614. An EcoRI digest of C614

produced the EcoRI fragment from C614 containing the 35S promoter which was cloned into the EcoRI site of pUC8 (Vieira *et al.*, Gene (1982) 19:259) to produce pCGN146. To trim the promoter region, the BglII site 5 (bp 7670) was treated with BglII and Bal31 and subsequently a BglII linker was attached to the Bal31 treated DNA to produce pCGN147.

pCGN148a containing the promoter region, selectable marker (KAN with 2 ATGs) and 3' region was 10 prepared by digesting pCGN528 (see below) with BglII and inserting the BamHI-BglII promoter fragment from pCGN147. This fragment was cloned into the BglII site of pCGN528 so that the BglII site was proximal to the kanamycin gene of pCGN528.

The shuttle vector used for this construct, pCGN528, was made as follows. pCGN525 was made by digesting a plasmid containing Tn5 which harbors a kanamycin gene (Jorgenson *et al.*, Mol. Gen. (1979) 177:65) with HindIII-BamHI and inserting the HindIII-BamHI fragment containing the kanamycin gene into the HindIII-BamHI sites in the tetracycline gene of pACYC184 (Chang and Cohen, J. Bacteriol. (1978) 134: 1141-1156). pCGN526 was made by inserting the BamHI fragment 19 of pTiA6 (Thomashow *et al.*, Cell (1980) 25:19:729-739) into the BamHI site of pCGN525. pCGN528 was obtained by deleting the small XhoI fragment from pCGN526 by digesting with XhoI and religating.

pCGN149a was made by cloning the BamHI kanamycin gene fragment from pMB9KanXXI into the BamHI site 30 of pCGN148a. pMB9KanXXI is a pUC4K variant (Vieira and Messing, Gene (1982) 19:259-268) which has the XhoI site missing but contains a functional kanamycin gene from Tn903 to allow for efficient selection in Agrobacterium.

pCGN149a was digested with BglII and SphI. 35 This small BglII-SphI fragment of pCGN149a was replaced with the BamHI-SphI fragment from MI isolated by digestion with BamHI and SphI. This produces pCGN167.

(f) Construction of pCGN766c (35S promoter-3' region)

The HindIII-BamHI fragment of pCGN167 containing the CaMV-35S promoter, 1 ATG-kanamycin gene and the 5 BamHI fragment 19 of pTiA6 was cloned into the BamHI-HindIII sites of pUC19 (Norlander et al., supra (1985); Yanisch-Perron et al., supra (1985)) creating pCGN976.

The 35S promoter and 3' region from transcript 7 was developed by inserting a 0.7 kb HindIII-EcoRI 10 fragment of pCGN976 (35S promoter) and the 0.5 kb EcoRI-SalI fragment of pCGN709 (transcript 7:3' for construction see supra) into the HindIII-SalI sites of pCGN566 creating pCGN766c.

15 (g) Final Construction of pCGN783

The 0.7 kb HindIII-EcoRI fragment of pCGN766c (CaMV-35S promoter) was ligated to the 1.5 kb EcoRI-SalI fragment of pCGN726c (1-ATG-KAN-3' region) into the HindIII-SalI sites of pUC119 (J. Vieira, Rutgers 20 University, New Jersey) to produce pCGN778. The 2.2 kb region of pCGN778, HindIII-SalI fragment containing the CaMV 35S promoter (1-ATG-KAN-3' region) replaced the HindIII-SalI polylinker region of pCGN739 to produce pCGN783.

25 The mas-levansucrase cassette pCGN1201 was inserted into the unique SalI site of pCGN783 to create plasmid pCGN1205. This plasmid in E. coli C2110 is conjugated into Agrobacterium strain PC2760 (Ooms et al., Plasmid (1982) 7:15-29; Hoekema et al., Nature (1983) 30 303:179-181; European Patent Application 84-200239; 2424283) which contains a disarmed Ti-plasmid, using gentamicin selection.

Example 5
Construction of Dextranucrase
Expression Cassettes

5

Expression of Cassettes Generally

The dextranucrase gene from pCGN1222 was cloned through a series of steps into pCGN2306 (Figure 8). The dextranucrase gene was then removed from pCGN2306 as an EcoRV fragment and cloned into the respective promoter cassettes (pCGN2305, having the 35S CaMV promoter and pCGN1241, having the 2A11 promoter). The resulting constructs were then cloned into a binary cassette (pCGN1547) in both orientations, yielding a total of 4 constructs, pCGN2318 and 2319 and pCGN2310 and 2311 (Figure 9).

2A11 Promoter Cassette

The design of the 2A11 cassette (pCGN1241) is shown in Figure 7. The cassette contains 3.8 kb of DNA 5' of the transcriptional start site and the entire 3' region (from the TGA stop codon to a site 2.0 kb 3' of the poly A addition site) of the 2A11 gene. A map of the 2A11 gene is shown in Figure 6, showing the restriction sites and indicating (below the representation of the gene) the regions of the 2A11 gene used to construct the 2A11 cassette. The 2A11 cassette was constructed as follows.

The 5' end of the 2A11 cassette was constructed starting with an EcoRI subclone genomic clone as described in application PCT/US88/01811 cloned into the EcoRI site of Bluescript (+) (Stratagene) resulting in pCGN1288. This clone contains sequences from the EcoRI site at position 1651 in the intron of the 2A11 gene to the EcoRI site located 2.5 Kb upstream 35 of the XhoI site at position 1 of the sequenced region (see Figure 6). The XhoI fragment from position 1 of the sequenced region to the XhoI site in the Bluescript

polylinker was deleted creating plasmid pCGN2004 which contains the 2AII region from position 1 to position 1651. The coding region of 2AII was deleted by treating this plasmid with ExonucleaseIII/S1 (using the commercially available Erase-a-Base Kit (Promega Biotec)) and sequencing deletion plasmids until one was found which had the coding region deleted to position 1366. The resulting plasmid, pCGN1251, had the genomic region from the XhoI site (position 1) to position 1366. The EcoRI fragment of pCGN1288 was then transferred to a chloramphenicol resistant plasmid vector, pCGN2015, to make pCGN1231. pCGN2015 is a Cm resistant derivative of the Bluescript plasmid. A BstEII/BamHI fragment of pCGN1251 was then transferred into BstEII/BamHI digested pCGN1231 to make pCGN1235 which contains the region from the EcoRI site (2.5 kb upstream of the sequenced region) to position 1366 of the sequenced region flanked by the Bluescript polylinker in a Cm resistant vector.

The 3' end of the 2AII cassette was constructed from pCGN1273 (described in application PCT/US88/01811) by digesting the plasmid with PvuI and EcoRI, isolating the 2249 bp insert (from position 2402 to 4653), ligating with a double-stranded oligonucleotide containing the sequence shown in Figure 6 from the BamHI sticky end to a PvuI sticky end into a Bluescript vector which had been digested with BamHI and EcoRI. The resulting plasmid, pCGN1238 contains the 3' end of the 2AII gene from the stop codon at position 2381 to the EcoRI site at position 4653.

A cassette containing the 5' and 3' regions of the 2AII gene was constructed by ligating the BamHI to EcoRV insert of pCGN1238 into pCGN1235 which had been digested with BamHI and XbaI (the XbaI site having been filled in with Klenow polymerase to make a blunt-ended fragment). The resulting plasmid, pCGN1240, has the 5' end of the 2AII gene from the EcoRI site 2.5 kb

upstream of the XhoI site (position 1) to position 1366 (which is located between the transcriptional initiation site of the 2A11 gene and the ATG), followed by a polylinker region (sequence given in Figure 6)

5 with sites for SmaI, BamHI, PstI and SalI which can be conveniently used to insert genes followed by the 3' region from position 2381 to 4653. The plasmid backbone of pCGN1240 is the Bluescript Cm plasmid described above. A more convenient version has the

10 EcoRI of 1240 excised and inserted into a Bluescript vector with an altered polylinker from the SacI site to the KpnI site with a synthetic polylinker with the following sequence:

AGCTCGGTACCGAATTCTGAGCTCGGTAC to create a
15 polylinker with the following sites: SacI-KpnI-SacI-KpnI. The EcoRI insert of pCGN1240 was inserted into pCGN1240 to make pCGN1241 (Figure 7).

35S Promoter Cassette

20 The 35S CaMV cassette (pCGN2305) contains DNA 5' of the transcriptional start site of the 35S CaMV gene of the 3' region of the Tr7 gene. It was constructed as follows. pCGN1410 (Sheehy et al., (1988) Proc. Natl. Acad. Sci. (USA), 85:8805-8809) is
25 digested with EcoRI, and the ends filled in with DNA polymerase I. A phosphorylated XbaI linker from Pharmacia, 5'-pd[TCTAGA]-3' is ligated in. The resulting plasmid was called pCGN2304. pCGN2304 was then digested with HindIII, the ends filled in with DNA
30 polymerase I, and a phosphorylated XbaI linker ligated in. The resulting plasmid was called pCGN2305.

Preparation of Necessary Constructs

pCGN2302. The 3' end of the gene was subcloned from pCGN1222 (see Example 3) as a 3.1 kb
35 SalI/EcoRV fragment into pCGN2015 to give pCGN2302. The plasmid pCGN2015 was constructed by digesting

pCGN565 with HhaI blunting with mung bean nuclease and ligating with EcoRV digested Bluescript KSM13 (Stratagene, San Diego, CA) to create pCGN2008.

5 pCGN565 is a cloning vector based on pUC8-pUC13-cm (K. Buckley (1985), supra) but containing pUC18 linkers (Yanisch-Perron et al., Gene (1985) 53:103-119).

pCGN2008 was digested with EcoRI and HindIII, blunted with Klenow. The 1156 bp chloramphenicol fragment was isolated. Bluescript KSM13+ (Stratagene) 10 was digested with DraI and the 2273 bp fragment is isolated and ligated with the pCGN2008 chloramphenicol fragment creating pCGN2015.

15 pCGN2306. The remaining 1.6 kb 5' end of the dextranase gene was generated using the polymerase chain reaction method, Tag polymerase (Gene Amp kit) and the DNA thermal cycler (Perkin-Elmer Cetus) using pCGN2023 as a template. pCGN was made by a BamHI deletion of pCGN1222. Two oligonucleotides, Dex02 (42-mer with the added restriction sites, XhoI and EcoRV 20 upstream of the ATG codon, plus sequence complementary to the ATG region) and Dex03 (a 26-mer complimentary to the SalI region) were used as primers. Dex02: 5'-GGTTATCTCGAGGATATCATGCCATTACAGAAAAGTAATG-3'
Dex03: 5'-CAAATCAGCATCCACATTGTCGACTG-3'

25 The resulting 1.6 kb fragment contains the 5' end of the gene, from the ATG start codon through the SalI site with an additional ShoI site and an EcoRV site upstream of the ATG. The 1.6 kb fragment was then cloned in pCGN2303 as an XhoI/SalI fragment, in front 30 of the 3' end of the gene giving plasmid pCGN2306.

35 pCGN1547. pCGN1547 (described in co-pending U.S. patent application Serial No. 329,018, (which disclosure is hereby incorporated by reference) is a binary plant transformation vector containing the left and right T-DNA borders of Agrobacterium tumefaciens octopine Ti-plasmid pTiA6 (Currier and Nester, J. Bact. (1976) 126:157-165), the gentamycin resistance gene of

pPH1JI (Hirsch and Beringer, Plasmid (1984) 12:139-141), an Agrobacterium rhizogenes Ri plasmid origin of replication from pLJbB11 (Jouanin et al., Mol. Gen. Genet. (1985) 201:370-141), the mas promoter region and 5 mas 3' region of pTiA6 with the kanamycin resistance gene of Tn5 (Jorgensen et al., Mol. Gen. Genet. (1979) 177:65), a ColE1 origin of replication from pBR322 (Bolivar et al., Gene 2:95-113), and a lacZ' screenable marker gene from pUC18 (Yannisch-Perron et al., Gene 33:103-119).

Final Construction Steps

The entire dextranase gene was removed from pCGN2306 as an EcoRV fragment and cloned as a blunt ligation into the SmaI sites of the promoter 15 cassettes pCGN2305, giving plasmid pCGN2309, and pCGN1241, giving pCGN2307. Each cassette was cloned into the binary vector pCGN1547 as an XbaI fragment for the 35S cassette to create pCGN2318 and pCGN2319, and as a KpnI fragment from the 2A11 cassette to create 20 pCGN2310 and 2311. This allows for constructs in both orientations for each cassette. The completed binaries were then submitted for cocultivation. Agrobacterium tumefaciens strain 2760 (also known as LBA 4404, Hoekema et al., Nature (1983) 303:179-180) were 25 transformed with the receptive binary using the method of Holsters et al. Mol. Gen. Genet. (1978) 163:181-187. The transformed binary was then used in the cocultivation of plants.

Example 6

Preparation of Transgenic Plants

Feeder plates were prepared by pipetting 0.5 ml of an eight day old suspension of Nicotiana tabacum cv xanthi cell suspension culture ($\sim 10^6$ cells/ml) onto 35 0.8% agar medium, containing MS salts, myo-inositol (100 mg/l), thiamine-HCl (1.3 mg/l), sucrose (30 g/l), potassium acid phosphate (200 mg/l) 2,4-D (0.2 mg/l),

and kinetin (0.1 mg/l) (pH 5.5). The feeder cells were prepared at least 24 hours prior to use. A #1 Whatman sterile filter paper (Whatman Ltd, Maidstone, England) was placed on top of the tobacco feeder cells after the 5 cells had been growing for at least 24 hours.

Agrobacteria containing the plasmid of interest were grown on AB medium (AB salts K_2HPO_4 3 gm/l, $NaH_2PO_4 \cdot H_2O$ 1.15 g/l, NH_4Cl 1 g/l, glucose 5 g/l, $FeSO_4$ 0.25 mg/l, $MgSO_4$ 0.246 mg/l, 0.14 mg/l, 15 g/l 10 agar 100 μ /l gentamycin sulfate and 100 μ /l streptomycin sulfate) for 4-5 days. Single colonies were then inoculated into 5 mls of MG/L broth and preincubated overnight in a shaker (180 rpm) at 30°C.

Sterile tomato cotyledon tissue was obtained 15 from 7-8 day old seedlings which had been grown at 24°C, with a 16hr/ 8hr day/night cycle in 100 x 25 mm petri dishes containing MSSV medium: Murashige-Skoog (MS) salts (#1117 Gibco Laboratories, New York), sucrose 30 g/l, Nitsch vitamins (Thomas, B.R., and 20 Pratt, D. Appl. Genet. (1981) 59:215-219), 0.8% agar (pH 6.0). Any tomato species may be used, however, the inbred breeding line UC82B (Department of Vegetable Crops, University of California, Davis) is preferred. The tips and bases of the cotelydons were removed and 25 the center section placed onto a feeder plate for a 24-hour preincubation period in a low light, 40-50 microEinsteins, but no greater than 80 microEinsteins, at 24°C.

Following the preincubation period, the 30 cotyledon explants were then dipped into the agrobacteria suspension (5×10^8 bacteria/ml) for approximately 5 minutes, blotted on sterile paper towels and returned to the original tobacco feeder plates. The explants were cocultivated with the 35 agrobacteria for 48 hours on the tobacco feeder plates in low light (see above) at 24°C, then transferred to regeneration medium containing 500 mg/l of carbenicil-

lin disodium salts and at least 100 mg/l of kanamycin sulfate. The regeneration medium is MS sa4s medium with zeatin (2 mg/l), myo-inositol (100 mg/l), sucrose (20 g/l), Nitsche vitamins and 0.8% agar (pH 6.0).

5 After 10 days and subsequently every three weeks, the explants were transferred to fresh regeneration medium containing 500 mg/l of carbenicillin disodium salts and at least 100 mg/l of kanamycin sulfate. Shoots were harvested from 8 weeks onwards and placed on MSSV
10 medium containing carbenicillin (50 mg/l), kanamycin (50 mg/l) and indole-3-butyric acid (1 mg/l). Roots developed in 7-14 days. Plants were then transplanted into soil.

15

Example 7
Targeting to Apoplast

The hydropath plot of the deduced amino acid sequence of the Leuconostoc dextranase shows a highly hydrophilic protein with a hydrophobic N-terminal region. As seen with many other gram-positive secreted proteins, the N-terminal sequence displays characteristics expected of a signal peptide. However, because these sequences are quite different from those seen for eukaryotic secretory proteins, it is possible that a heterologous leader sequence will be desired for efficient translocation of the sucrase enzyme to a desired cell organelle.
30 Various constructs therefore have been designed to optimize targeting of dextranase to the fruit apoplast.

PG/Dextranase Constructs

35 Constructs using the full-length dextranase gene as well as various 5' deletions of the gene were fused to either the full length polygalacturonase

(PG) leader (3141bp) or the 5' region of the polygalacturonase leader (146 bp). A new dextranuclease construct was made using the polymerase chain reaction (PCR) method. A 1.6 kb XhoI-SalI fragment of pCGN1222 was synthesized and inserted into XhoI digested pCGN2303 to make plasmid pCGN2327. This new construct, pCGN2327, Figure 10, is identical to pCGN2306 but lacks the EcoRV site at the 5' end.

Constructs containing the PG leaders fused to dextranuclease were prepared as follows: The full length PG leader fragment was cloned as a 314 bp XhoI-SalI PCR fragment into the XhoI site of pCGN2327 to give pCGN2330. The 5' PG leader fragment was cloned as a 146 bp XhoI-SalI PCR fragment into the XhoI site of pCGN2327 to give pCGN2331 (Figure 11). Other constructs having either the full-length or a shorter 5' fragment of the PG-leader are fused to the relevant sucrase genes in a like manner. Where it is desirable, for example, to delete 5' bacterial transit peptide regions, portions of the sucrase gene can be deleted to increase activity of the encoded protein. Once the construct is prepared having the desired truncations and/or deletions, the PG leader/dextranuclease regions can then be cloned into the 2A11 and 35S promoter cassettes (pCGN1241 and pCGN2305 respectively) and then into the binary plasmid 7, or other such constructs.

The resulting binary plasmid having the desired constructs therein are used to transform A. tumefaciens and through Agrobacterium-mediated transformation, to obtain transgenic plants.

Example 8
Analysis of Constructs
Comprising Transit Peptides

5 Two PG leader/GUS constructs were made to
study the targetting of dextran sucrase. The two
constructs, pCGN2313 (full length PG leader) and
pCGN2325 (5' PG leader) (Fig. 13), were electroporated
into tobacco protoplasts and all fractions (media, cell
10 wall debris, and protoplast) were assayed for GUS
activity. (Jefferson *et al.* Plant Molec. Biol. Rep.
(1987) 5:387-405.) In initial studies, no GUS activity
was detected in any fraction. The GUS gene contains
two glycosylation sites. It has been proposed that
15 glycosylation of GUS at one or more of these sites
during processing may inactivate the enzyme.
Therefore, the electroporation studies were repeated
using the antibiotic tunicamycin, which interferes with
glycoprotein biosynthesis and prevents glycosylation of
20 GUS. Data from these studies (Table 9) show that when
tunicamycin is added, GUS activity is retained and
glycosylation appears blocked. Since glycosylation of
proteins occurs between the endoplasmic reticulum and
the Golgi, the PG leader, full length as well as 5'
25 only, appears to be successfully taking the GUS protein
into the secretory pathway. This is also supported by
the fact that the GUS activity is reaching the cell
wall fraction of the electroporated protoplasts.
Western analysis of the protoplast fractions will be
30 used to verify these results.

Table 9¹GUS Activity In
Electroporated Protoplasts

	Construct	Without Tunicamycin Cell Wall		With Tunicamycin Cell Wall	
		Protoplast	Debris	Protoplast	Debris
10	pBl221 ²	28840	471	23450	431
		20250	214	17500	309
15	pCGN2313	990	104	25700	9590
		940	70	27400	5475
20	pCGN2325	2660	192	59100	9990
		1180	101	58300	14070

¹GUS activity is assayed as described by Jefferson et al. (supra). Activity is reported as fluorescence/180 min. reaction/electroporation (fluorescence units at 365 nm excitation/455 nm emission).

²pBl221 is a 35S/GUS construct used as a positive control.

20

Analysis of PG Leader-DextranucraseTransformed Tissue

Localization of dextranucrase in the apoplast of the tomato fruit can be determined by various methods. One such method is tissue printing of the fruit onto nitrocellulose paper (Cassab and Varner, (1987) J. Cell. Biol., 105:2581-2588). In this procedure a transformed tomato fruit is sliced, washed briefly in distilled water, quickly dried and blotted onto nitrocellulose paper that has previously been soaked in 0.2M CaCl₂ and dried. The tissue print is then immediately dried and treated for the detection of dextranucrase using alkaline phosphatase-conjugated second antibody as follows. The nitrocellulose blot is incubated in a blocking buffer consisting of 50 mM Tris-HCl, pH7.5, 200mM NaCl, 0.05% Tween-20 (TTBS) and

1% bovine serum albumin, then incubated in rabbit antidextranase antibody in TTBS. Biotinylated goat anti-rabbit IgG is then bound followed by incubation in streptavidin-alkaline phosphatase conjugate. BCIP (5-bromo-4-chloroindoxyl phosphate) and NBT (nitroblue tetrazolium) are used as substrate to visualize the precipitated indoxyl group. Individual cells on the tissue print are then examined under a dissecting microscope for localization of dextranase.

Another method used to locate dextranase in transformed tomato fruit is immunofluorescence (Vreeland *et al.*, (1984), Planta., 162:506-517) or immunogold (Mauch and Staehelin, (1989), Plant Cell., 1:447-457, Dorel *et al.*, (1989), J. Cell Biol., 108:327-337, Cassab and Varner, (1987), J. Cell Biol., 105:2581-2588) labelling of antigen in thin tissue sections by dextranase polyclonal antibody. Transformed tomato fruit are dissected under fixative conditions appropriate for either light or electron microscopic immunocytochemistry (Greenwood and Chrispeels, (1985), Plant Physiol., 79:65-71). Thin sections of the fruit (0.05-1 μ m) then are cut from the fixed tissue, mounted on slides and processed for immunocytochemistry by either immunofluorescence or immunogold labelling techniques. The labelled thin sections are then analyzed under appropriate microscopic conditions for the localization of dextranase.

30

Example 9Analysis of Transgenic PlantsNPT II Enzyme Assay

Leaves from plants transformed with a construct of interest which regenerated from kanamycin-resistant explant tissue were assayed for expression of the NPT II gene. Tissue was harvested, frozen in

liquid nitrogen, ground frozen in Eppendorf tubes containing equivalent amounts (w/v) of extraction buffer (2.5 mM Tris-HCl, pH 6.8, 0.143 mM β -mercaptoethanol, 0.27 mM leupeptin) then centrifuged for 15 min.

5 The supernatant from leaf homogenates was added to half volume aliquots of reaction buffers A and B. Reaction buffer A contained 67 mM Tris-maleate, 42 mM MgCl₂, 400 mM NH₄Cl, 1.7 mM dithiothreitol, 0.4 mg/ml kanamycin sulfate. Reaction buffer B was identical to buffer A, except that kanamycin was omitted. [γ -³²P] ATP solution (0.75 mM ATP dissolved in reaction buffer B and 1.0 μ Ci [γ -³²P] ATP/sample) was added to each reaction mixture. The samples were incubated at 32°C for 30 min. Using a slot blotting apparatus, reaction samples were blotted onto three layers of Whatman P81 ion exchange papers placed on top of one Whatman 3mm paper. All three P81 papers were washed twice with water at 25°C for 4 min each. The blots were incubated for 45 min at 65°C in proteinase K solution (1.0 mg/ml proteinase K in 1% SDS), then washed once at 80°C for 4 min followed by a wash at room temperature. After drying, blots were exposed to X-ray film with an intensifying screen.

25 Northern Analysis

Out of 19 transformed plants containing the levansucrase construct, and 2 transformed plants containing the 2All/dextran sucrase construct, and 42 transformed plants containing the 355/dextran sucrase construct, 14, 41 and 35 plants, respectively, show expression the kan gene.

Isolation of Poly(A)⁺ RNA

Leaves and fruit (green as well as ripe) from 35 transformed tomato plants were harvested and frozen in liquid nitrogen. Frozen leaves were ground in a mortar and pestle in liquid nitrogen and total RNA was extracted.

ted from the resulting powder by homogenization in Tris-HCl, SDS buffer and lithium chloride precipitation as described by Crouch *et al.*, J. Mol. Appl. Gen. (1983) 2:273-283. Frozen ripe fruit was ground to a powder in 5 a mortar and pestle in liquid nitrogen and homogenized with a Brinkmann polytron continuously for 2 min on ice. Total RNA is isolated as described by Colbert *et al.*, Proc. Natl. Acad. Sci. (1983) 80:2248-2252 using the extraction buffer described by Facciotti *et al.*, 10 Bio/Tech (1985) 3:241-246 and pelleted through a high-density CsCl solution on a Beckman type 60Ti rotor as described by Turpen and Griffith, BioTechniques (1986) 4:11-15. Poly(A)⁺ RNA is isolated as described by Maniatis *et al.* (1982). Contaminating sucrases are 15 removed from the samples by washing with Sigmacell^R type 50 in 20 mM Tris-HCl, pH 7.5, 0.5 M NaCl, 1 mM EDTA, 0.1% SDS.

RNA Probe Preparation

20 A ³²P-labeled RNA probe complementary to the gene of interest is synthesized using a Riboprobe kit (Promega Biotech), according to the manufacturers instructions, and labeling with $\alpha^{32}\text{P}$ -rUTP, according to the manufacturer's instructions. The probe to the levansucrase gene was 25 synthesized from the T7 promoter of the plasmid pCGN499 (see supra).

Analysis

mRNA isolated from leaves of transformed plants 30 is denatured and electrophoresed as described by Shewmaker *et al.*, Virology (1985) 140:281-288. The gels were blotted overnight against 20x SSC (3 M sodium chloride, 0.3 M sodium citrate, pH 7.0) the nitrocellulose filters baked at 80°C for 2 hrs and then hybridized at 50°C in the 35 hybridization buffer suggested by the Riboprobe manufacturer containing 0.5 mg/ml denatured yeast tRNA, 0.5 mg/ml denatured salmon sperm DNA, and 0.25 mg/ml polyanethole-

sulfonic acid. Blots are then washed at 55°C for 30 min and twice at 65°C for 30 min each in buffer as described by the Riboprobe manufacturer. Contaminating ribosomal RNA is removed from the blots by washing them with 1 µg/ml 5 ribonuclease in 2x SSC at 25°C.

As shown in Figure 12, two of the transformed plants analyzed hybridized to the levansucrase probe, although only one of the constructs was producing a full length transcript. Analysis of mRNA from ripe fruit from 10 the transformants gave the same results.

Analysis of Tomato Fruit for Sucrase Activity

Protein is isolated from green fruit from a transformed plant, which appears from Northern analysis to 15 be producing a full length transcript of the gene of interest, and from green fruit of nontransformed Calgrande plants as a negative control. The method used is as follows. Fruit is frozen then allowed to thaw in 1.5 M NaCl, 0.1 M sodium citrate, pH 6 buffer, ground in a 20 mortar and pestle, then homogenized using a Polytron for 3 min at 4°C. Large debris is removed by centrifugation twice at 5500 x g. The supernatant is then brought to 95% 25 (NH₄)₂SO₄. After stirring for 1 hr at 4°C the samples are centrifuged and the protein precipitate is resuspended in 10 ml of 0.05 M KPO₄ buffer, pH 5. The samples are then dialyzed overnight against 0.05 M KPO₄, pH 6, centrifuged to remove any precipitants and the supernatant analyzed 30 for levansucrase activity.

Levansucrase was isolated from Bacillus subtilis strain QB118 as described by Dedonder, Methods in Enzymol. (1966) 30:500-505. Briefly, the supernatant from a one-liter 35 14-hr culture grown in EcLB (5 g/l yeast extract, 10 g/l tryptone, 5 g/l NaCl) containing 10 g/l glucose at 30°C was isolated and pH adjusted to 4.2 by addition of acetic acid. Cold ethanol (2-4°C) was gradually added to 48% and stirred continuously at 4°C for 20 min then centrifuged to pellet the proteins. The pellet was dissolved

in 30 ml of 0.05 M KPO₄ and dialyzed overnight against 50% (NH₄)₂SO₄, pH 5, at 4°C overnight. The sample was then centrifuged and the supernatant dialyzed against 65% (NH₄)₂SO₄, pH 5, at 4°C overnight. Again the sample was 5 centrifuged and the supernatant was dialyzed against 95% (NH₄)₂SO₄, pH 5, at 4°C overnight. The sample was then centrifuged to pellet the proteins and the pellet was resuspended in 5 ml of 0.05 M KPO₄, pH 6, and dialyzed against 0.05 M KPO₄, pH 6, at 4°C overnight.

10 Dextranucrase process a radioactive polymer only from sucrose labelled in the glucose molecule of sucrase, while levansucrase produces a radioactive polymer only from sucrose labeled in the fructose molecule of sucrose. The protocol for listing labelled [glucose-¹⁴C] 15 as required in analysis of dextranucrase is discussed above. 50 µl of the supernatant obtained as above was added to reaction tubes containing 0.1µCi of dried sucrose [fructose-¹⁴C] and 50µl of reaction buffer (0.05M KPO₄, pH6, 0.01M sucrose, 20mg/ml levan (10,000 MW). The 20 reaction tubes were incubated at 30°C and sampled at various times for the incorporation of ¹⁴C into polymer by spotting aliquots of each reaction onto Whatman No. 1 filter paper. The filters were then washed in methanol as described supra for analysis of dextranucrase.

25 The above results demonstrate that plant species can be transformed efficiently with expression cassettes which provide for expression of a heterologous gene for a carbohydrate polymer synthesizing enzyme such as a bacterial dextran or levansucrase. As evidenced by the 30 above disclosure, plant species are provided which express a bacterial levansucrase or dextranucrase gene and as a result may have modified solids content without adverse effects on the normal production capabilities of the plant.

35 All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this

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invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to
5 be incorporated by reference.

The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the appended claims.

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WHAT IS CLAIMED IS:

1. A method for modifying the soluble solids composition of a plant cell, said method comprising:

5 growing plant cells comprising at least one copy of a foreign gene encoding an enzyme capable of polymerizing a carbohydrate comprising at least one hexose moiety to form a polymer under conditions whereby said gene is expressed and the soluble solids composition of said plant cells is modified.

10 2. The method according to Claim 1, wherein said carbohydrate is sucrose.

15 3. The method according to Claim 2, wherein said enzyme is dextranucrase or levansucrase.

4. A method for modifying the soluble solids composition of fruit, said method comprising:

20 growing a plant comprising cells containing at least one copy of an expression cassette comprising, in the 5'-3' direction of transcription, a transcriptional and translational initiation region active in a fruit cell, a DNA sequence encoding an enzyme capable of polymerizing a carbohydrate comprising at least one hexose moiety to form a polymer, wherein expression of said DNA sequence is regulated by said initiation region, and translational and transcriptional termination regions functional in a plant cell, under conditions whereby said 25 DNA sequence is expressed and the soluble solids composition of said fruit is modified.

30 35 5. A plant cell capable of producing sucrase at an enhanced level, said cell comprising:

at least one copy of a sucrase gene, wherein said cell was obtained by inserting into said cell, or a parent of said cell, an expression cassette, prepared in vitro,

comprising a sucrase gene under the transcriptional and translational control of transcriptional and translational initiation and termination regulatory regions functional in said cell.

5

6. The plant cell according to Claim 5, wherein said sucrase gene is a levansucrase gene or a dextran sucrase gene.

10

7. The plant cell according to Claim 5, wherein said plant cell is a fruit cell or a seed cell.

8. The plant cell according to Claim 6, wherein said plant cell is a tomato plant cell.

15

9. A plant producing increased levels of sucrase, said plant consisting essentially of:
cells obtained by inserting into said cells, or parents of said cells, an expression cassette, prepared in vitro, comprising a sucrase gene under the transcriptional and translational control of transcriptional and translational initiation and termination regulatory regions functional in said cells, whereby said cells produce increased levels of sucrase.

25

10. The plant according to Claim 9, wherein said sucrase gene is a levansucrase gene or a dextran sucrase gene.

30

11. A tomato plant comprising cells producing levansucrase or dextran sucrase.

12. The plant according to Claim 11, wherein said cells are fruit cells.

35

13. An expression cassette comprising a transcriptional and translational region functional in a

plant cell, a DNA sequence encoding levansucrase, and a transcriptional termination regulatory functional in a plant cell.

5 14. A plant cell comprising an expression cassette of Claim 13.

10 15. A DNA fragment at least substantially homologous with a DNA sequence encoding dextranase obtainable from L. mesenteroides.

15 16. A DNA fragment comprising L. mesenteroides dextranase structural gene.

17. A DNA fragment comprising the DNA sequence shown in Figure 4.

20 18. The DNA fragment according to any one of Claims 15, 16, or 17, wherein said fragment is joined to a heterologous DNA sequence.

25 19. A DNA construct comprising a DNA sequence encoding dextranase obtainable from L. mesenteroides joined to a heterologous DNA sequence.

20 20. The DNA construct according to Claim 19, wherein said heterologous DNA sequence is a transcriptional and translational initiation region functional in a plant cell.

30 21. The DNA construct according to Claim 20, wherein said transcriptional and translational initiation region is active at or immediately after anthesis and during fruit ripening.

35 22. The DNA construct according to Claim 21, wherein said initiation region is the 2AII initiation region.

23. An expression cassette comprising:
in the 5'-3' direction of transcription, a transcriptional
and translational region derived from 2A11; a first DNA
5 sequence encoding dextranucrase or levansucrase, and a
transcriptional and translational termination regulatory
region functional in a plant cell.

24. An expression cassette according to Claim
10 23, further comprising:

a second DNA sequence encoding a transit peptide
joined in reading frame at the 5' terminus of said first
DNA sequence, wherein said second DNA sequence is derived
from a gene encoding an apoplast polypeptide.

15

25. An expression cassette according to Claim
24, wherein said apoplast polypeptide is tomato poly-
galacturonidase.

20

26. A cell comprising a DNA construct according
to Claim 25.

27. The cell according to Claim 26, wherein said
cell is a plant cell.

25

28. The cell according to Claim 27, wherein said
plant cell is in vivo.

30

29. The cell according to Claim 28, wherein said
plant is tomato.

30. The cell according to Claim 29 comprising:
a DNA construct according to any one of Claims
20, 21, 22, 23, 24, and 25.

31. A polypeptide comprising:
a sucrase joined to a plant apoplast transit
peptide sequence.

5 32. The polypeptide according to Claim 31,
wherein said sucrase is dextranucrase or levansucrase.

10 33. The polypeptide according to Claim 32,
wherein said dextranucrase is L. mesenteroides
dextranucrase.

34. The polypeptide according to Claim 31,
wherein said plant apoplast transit peptide sequence is
derived from tomato polygalacturonase.

15

20

25

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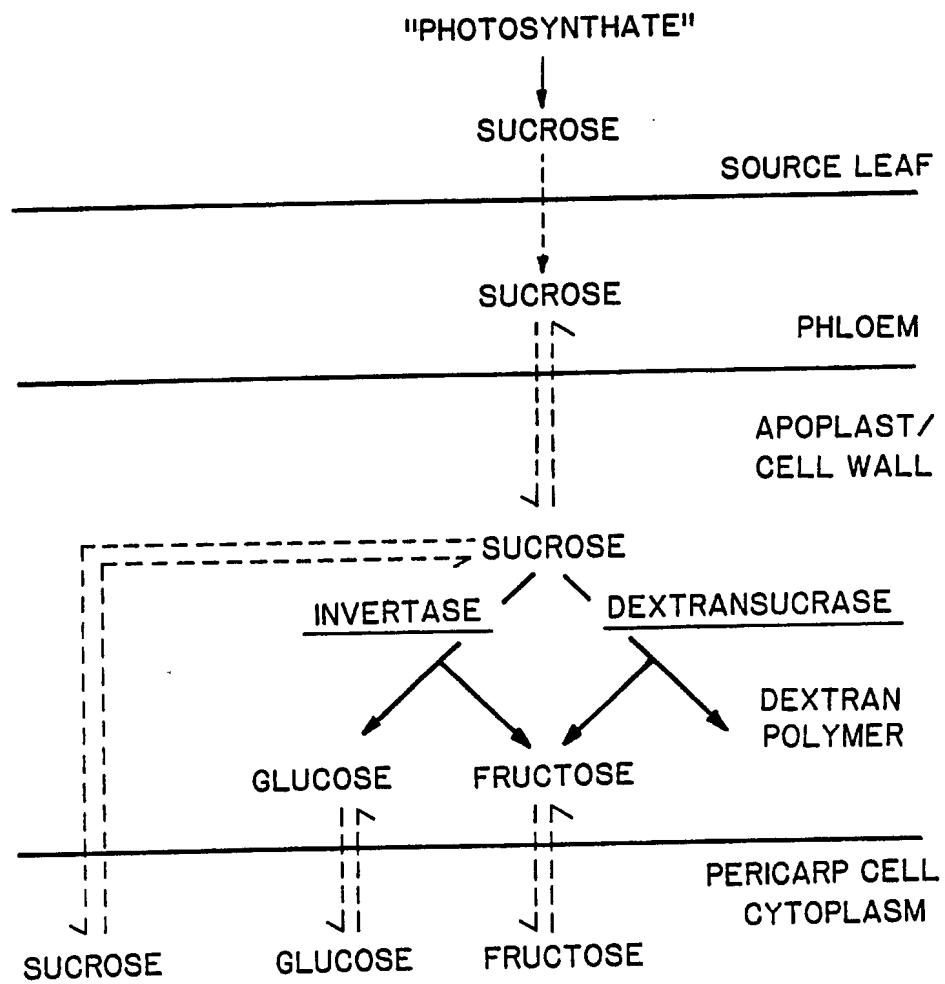
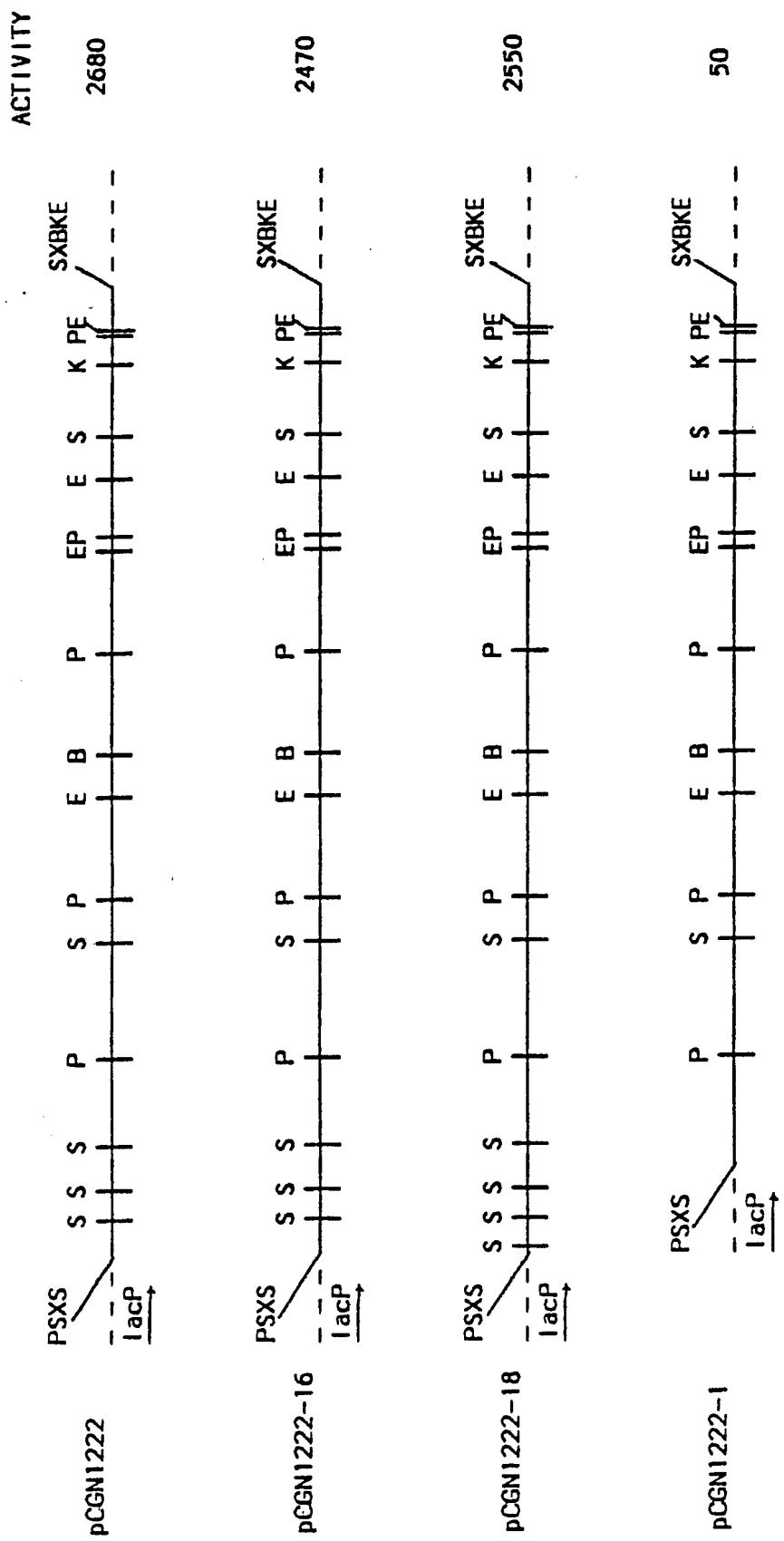


FIG. 1

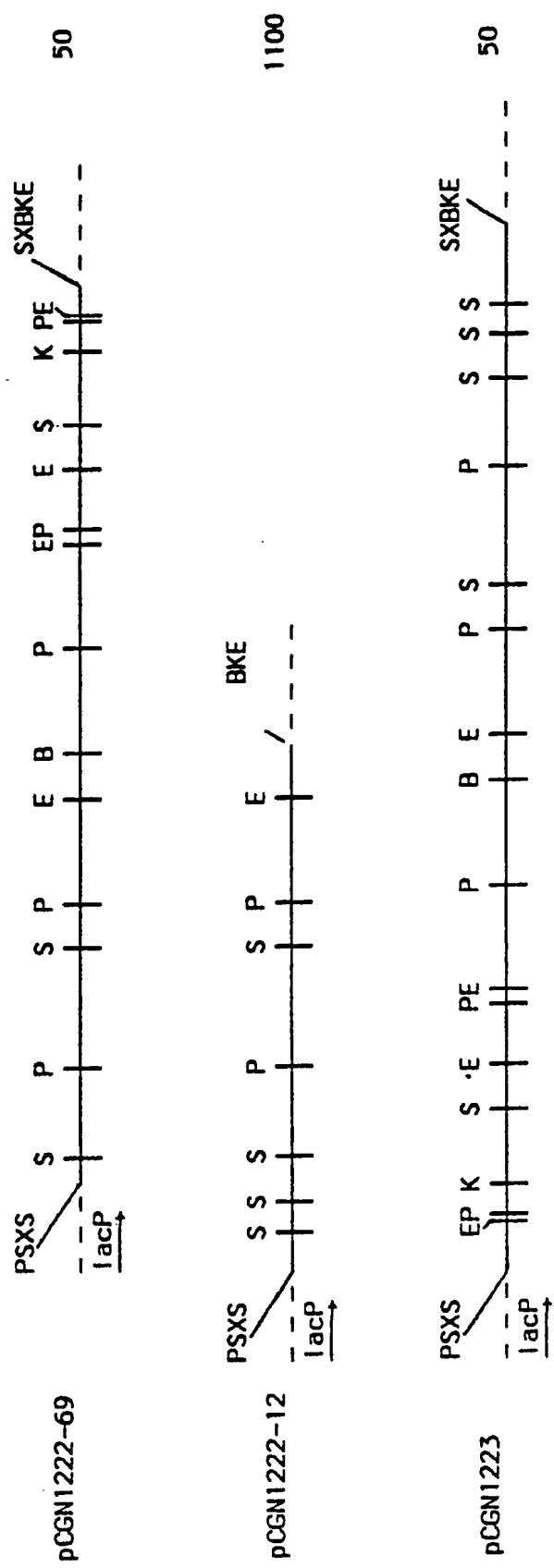
2/20

FIG. 2-1

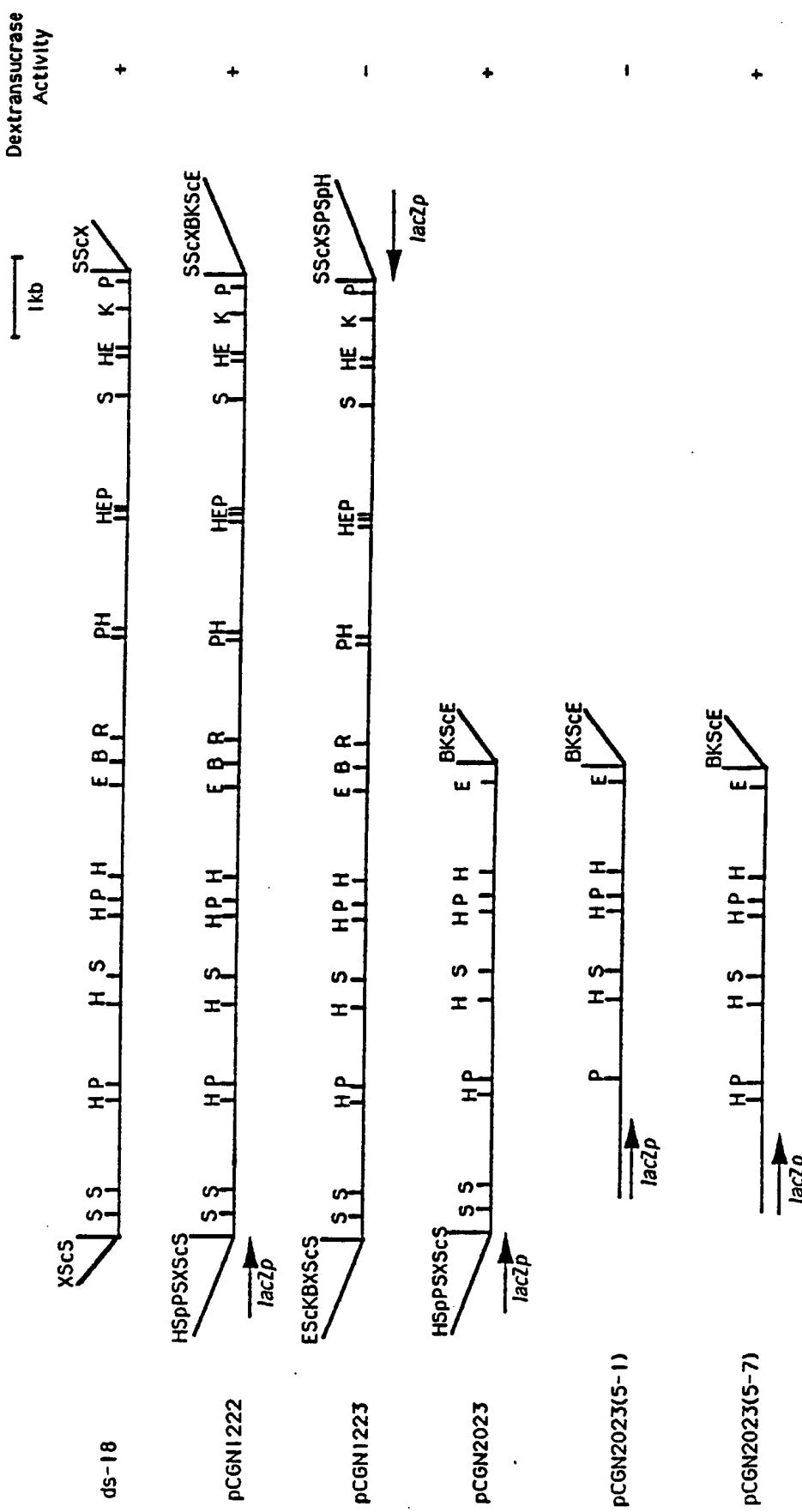


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FIG. 2-2



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FIG. 3

AATAAAATTAAATGACTAAATTAAATAACATTGTTAACCTTACAGATAAGTTAACATGTTTTT 71
 TTATAAAAATTAAATGTTTATAATTAAATAATTCTCTGATTGACTGTGTTTACAAATGTTTTTAATAA 142
 ATATGTCGATTGTGTATGAAATTTCATTACTGTTTACAATAATTAAAGTTAACATGTTAACATGTTATAA 213

-35	-10	5 / 20
GAAGAGAAATATAAGGAGAAATT ATG CCA TTT ACA GAA AAA GTA ATG CGG AAA AAG 273		
SD	M P F T E K V M R K K	
CTT TAT AAA GTT GGG AAA AGT TGG GTA GTT GGG GGT TGT GCT TTT GCA TTA 327		
L Y K V G K S W V V G G V C A F A L		
ACC GCC TCA TTT GCT TTA GCA ACA CCA AGT GTT TTA GGA GAC AGT AGT GCA CCT 381		
T A S F A L A T P S V L G D S V P		
GAT GTG AGT GCG AAT AAC GTT CAA TCT GCT TCA GAT AAT ACA ACG GAT ACG CAG 435		
D V S A N N V Q S A S D N T T D T Q		
CAG AAC ACT ACG GTT ACC GAA GAA AAT GAT AAA GTA CAG TCT GCA GCT ACT AAT 489		
Q N T T V T E E N D K V Q S A A T N		
GAC AAT GTA ACA ACA GCT GCA AGC GAC ACA ACA CAA TCT GCT GAT AAT GTG 543		
D N V T T A A S D T T Q S A D N N V		
ACA GAA AAA CAG TCA GAT GAT CAT GCA CTT GAT AAT GAA AAA GTC GAT AAC AAA 597		
T E K Q S D D H A L D N E K V D N K		
CAA GAT GAA GTC GCT CAA ACC AAT GTT ACT AGC AAA AAT GAG GAA TCA GCA GTT 651		
Q D E V A Q T N V T S K N E E S A V		
GCT TCA ACT GAC ACT GAT CCT GCT GAA ACG ACA ACT GAC GAA ACA CAA CAA GTT 705		
A S T D P A E T T D E T Q Q V		
AGC GGC AAG TAC GTT GAA AAA GAC GGT AGT TGG TAT TAT TTT GAT GAT GGC 759		
S G K Y V E K D G S W Y Y F D D G		
AAA AAT GCT AAA GGT TTA TCA ACG ATA GAC AAC AAT ATT CAA TAT TTT TAC GAG 813		
K N A K G L S T I D N N I Q Y F Y E		

FIG. 4-1

AGT	GGT	AAA	CAA	GCC	AAA	GGG	CAG	TAT	GTC	ACA	ATT	GAT	AAT	CAA	ACA	TAT	TAT	
S	G	K	Q	A	K	G	Q	Y	V	T	I	D	N	Q	T	Y	Y	
TTT	GAT	AAG	GGC	TCA	GGT	GAT	GAG	TTA	ACT	GGT	CTG	CAA	AGC	ATT	GAT	GGG	AAC	
F	D	K	G	S	G	D	E	L	T	G	L	Q	S	I	D	G	N	
ATA	GTT	GCT	TTT	AAC	GAT	GAA	GGG	CAA	CAA	ATT	TTT	AAT	CAA	TAT	TAC	CAA	TCT	
I	V	A	F	N	D	E	G	Q	Q	I	F	N	Q	Y	Y	Q	S	
GAA	AAT	GGT	ACA	ACA	TAC	TAC	TTT	GAT	GAT	AAA	GGA	CAC	GCT	GCT	ACC	GGT	ATT	
E	N	G	T	T	Y	F	D	D	K	G	H	A	A	T	G	I		
AAG	AAT	ATC	GAG	GGC	AAA	AAT	TAT	TAT	TTT	GAT	AAT	CTT	GGG	CAA	CTA	AAA	AAA	
K	N	I	E	G	K	N	Y	Y	F	D	N	L	G	Q	L	K	K	
GGC	TTC	TCT	GGT	GTG	ATT	GAT	GGT	CAA	ATA	ATG	ACA	TTT	GAT	CAG	GAA	ACA	GGG	
G	F	S	G	V	I	D	G	Q	I	M	T	F	D	Q	E	T	G	
CAA	GAA	GAA	TCT	TCT	AAC	ACA	ACT	TCT	GAA	ATA	AAA	GAA	GGT	TTG	ACG	ACT	CAA	AAC
Q	E	V	S	N	T	T	S	E	I	K	E	G	L	T	T	Q	N	
ACG	GAT	TAT	AGC	GAA	CAT	AAT	GCA	GCC	CAC	GGT	ACG	GAT	GCT	GAG	GAC	TTT	GAA	
T	D	Y	S	E	H	N	A	A	H	G	T	D	A	E	D	F	E	
AAT	ATT	GAC	GGC	TAT	TTA	ACA	GCT	AGT	TCA	TGG	TAT	CGT	CCA	ACA	GGT	ATT	TTA	
N	I	D	G	Y	L	T	A	S	S	W	Y	R	P	T	G	I	L	
CGT	AAC	GGA	ACA	GAC	TGG	GAA	CCT	TCT	ACA	GAT	ACA	GAT	TTC	AGA	CCA	ATA	TTG	
R	N	G	T	D	W	E	P	S	T	D	T	D	F	R	P	I	L	
TCA	GTG	TGG	TGG	CCA	GAT	AAG	AAC	ACC	CAG	GTC	AAT	TAT	TAA	TAC	ATG	GCT	1407	
S	V	W	W	P	D	K	N	T	Q	V	N	Y	L	N	Y	M	A	
GAT	TTA	GGG	TTT	ATC	AGT	AAT	GCG	GAC	AGT	TTT	GAA	ACT	GGG	GAT	AGC	CAA	AGC	
D	L	G	F	I	S	N	A	D	S	F	E	T	G	D	S	Q	S	
TTA	TTA	AAT	GAA	GCA	AGT	AAC	TAT	GTT	CAA	AAA	TCA	ATT	GAA	ATG	AAA	ATT	AGT	
L	L	N	E	A	S	N	Y	V	Q	K	S	I	E	M	K	I	S	
GCG	CAA	CAA	AGT	ACA	GAG	TGG	TTA	AAG	GAT	GCA	ATG	GCG	GCC	TTC	ATT	GTC	GCG	
A	Q	Q	S	T	E	W	L	K	D	A	M	A	F	I	V	A		
CAA	CCA	CAG	TGG	ATG	GAA	ACT	AGT	GAA	GAT	ATG	AGC	AAT	GAC	CAT	TTA	CAA	AAT	
Q	P	Q	W	N	E	T	S	E	D	M	S	N	D	H	L	Q	N	
GGC	GCA	TAA	ACT	TAT	GTC	AAC	AGT	CCA	CTG	ACA	CCT	GAC	GCT	AAT	TCA	AAC	TTT	
G	A	L	T	Y	V	N	S	P	L	T	P	D	A	N	S	N	F	

FIG. 4-2

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AGA	CTA	CTT	AAT	CGG	ACA	CCA	ACA	AAC	CAG	ACT	GGT	GAA	CAA	GCG	TAT	AAT	TTA	1731
R	L	N	R	T	P	T	N	Q	T	G	E	Q	A	Y	N	L		
GAT	AAT	TCA	AAA	GGT	TTT	GAA	TTG	TTG	TTA	GCC	AAT	GAC	GTT	GAT	AAT	TCA	1785	
D	N	S	K	G	F	E	L	L	A	N	D	V	D	N	S			
AAC	CCT	GTA	GTA	CAA	GCA	GAA	CAA	TTG	AAT	TGG	TTA	TAT	TAT	TTA	ATG	AAT	TTT	1839
N	P	V	V	Q	A	E	Q	L	N	W	L	Y	Y	L	M	N	F	
GGT	ACG	ATT	ACG	GCC	AAC	GAC	GCG	GAT	GCT	AAT	TTT	GAT	GGT	ATT	CGT	GTA	GAT	1893
G	T	I	T	A	N	D	A	D	A	N	F	D	G	I	R	V	D	
GCA	GTC	GAC	AAT	GTG	GAT	GCT	GAT	TTG	TTA	CAA	ATT	GCT	GCC	GAT	TAT	TTC	AAA	1947
A	V	D	N	V	D	A	D	L	Q	I	A	A	D	Y	F	K		
CTA	GCT	TAC	GGT	GTT	GAT	CAA	AAT	GAT	GCT	ACT	GCT	AAT	CAG	CAT	CTT	TCA	ATT	2001
L	A	Y	G	V	D	Q	N	D	A	T	A	N	Q	H	L	S	I	
TTG	GAA	GAT	TGG	AGT	CAC	AAT	GAT	CCT	TTG	TAT	GTA	ACA	GAT	CAA	GGA	AGC	AAT	2055
L	E	D	W	S	H	N	D	P	L	Y	V	T	D	Q	G	S	N	
CAA	TTA	ACC	ATG	GAT	GAT	TAT	GTG	CAC	ACA	CAA	TTA	ATC	TGG	TCT	CTA	ACA	AAA	2109
Q	L	T	[M]	D	D	Y	V	H	T	Q	L	I	W	S	L	T	K	
TCA	TCT	GAC	ATA	CGA	GGT	ACA	ATG	CAG	CGC	TTC	GTG	GAT	TAT	TAT	ATG	GTG	GAT	2163
S	S	D	I	R	G	T	M	Q	R	F	V	D	Y	Y	M	V	D	
CGA	TCT	AAT	GAT	AGT	ACA	GAA	AAC	GAA	GCC	ATT	CCT	AAT	TAC	AGC	TTT	GTA	CGT	2217
R	S	N	D	S	T	E	N	E	A	I	P	N	Y	S	F	V	R	
GCA	CAC	GAC	AGC	GAA	GTG	CAA	ACG	GTT	ATT	GCC	CAA	ATT	GTT	TCC	GAT	TTG	TAT	2271
A	H	D	S	E	V	Q	T	V	I	A	Q	I	V	S	D	L	Y	
CCT	GAT	GTT	GAA	AAT	AGT	TTA	GCA	CCA	ACA	ACA	GAA	CAA	TTG	GCA	GCT	GCT	TTC	2325
P	D	V	E	N	S	L	A	P	T	T	E	Q	L	A	A	A	F	
AAA	GTA	TAC	AAT	GAA	GAT	GAA	AAA	TTA	GCA	GAC	AAA	AAG	TAC	ACA	CAA	TAT	AAT	2379
K	V	Y	N	E	D	E	K	L	A	D	K	K	Y	T	Q	Y	N	
ATG	GCT	AGT	GCT	TAT	GGG	ATG	TTG	CTA	ACC	AAT	AAG	GAT	ACT	GTT	CCT	CGT	GTC	2433
M	A	S	A	Y	A	M	L	L	T	N	K	D	T	V	P	R	V	
TAT	TAT	GGC	GAT	TTA	TAT	ACA	GAT	GGT	CAA	TAT	ATG	GCA	ACA	AAG	TCA	CCA	2487	
Y	Y	G	D	L	Y	T	D	D	G	Q	Y	M	A	T	K	S	P	

FIG. 4-3

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TAC	TAT	GAT	GCG	ATT	AAC	ACT	TTG	CTA	AAG	GCT	AGA	GTT	CAG	TAT	GTT	GCT	GGT	2541
Y	Y	D	A	I	N	T	L	K	A	R	V	Q	Y	V	A	G		
GGC	CAA	TCG	ATG	TCC	GTT	GAT	AGT	AAT	GAC	GTG	TTA	ACA	AGT	GTT	CGC	TAT	GGT	2595
G	Q	S	M	S	V	D	S	N	D	V	L	T	S	V	R	Y	G	
AAA	GAT	GCC	ATG	ACA	GCT	TCT	GAC	ACT	GGA	ACA	TCT	GAG	ACG	CGT	ACT	GAA	GGT	2649
K	D	A	M	T	A	S	D	T	G	T	S	E	T	R	T	E	G	
ATT	GGA	GTC	ATC	GTC	AGC	AAT	AAC	GCG	GAG	CTA	CAA	TTA	GAG	GAT	GGG	CAT	ACT	2703
I	G	V	I	V	S	N	N	A	E	L	Q	L	E	D	G	H	T	
GTC	ACA	TTG	CAT	ATG	GGG	GCA	GCT	CAT	AAG	AAC	CAA	GCT	TAT	CGT	GCT	TTG	TTA	2757
V	T	L	H	M	G	A	A	H	K	N	Q	A	Y	R	A	L	L	
TCA	ACA	ACT	GCA	GAT	GGG	TGA	GCT	TAT	TAT	GAT	ACT	GAT	GAA	AAT	GCA	CCT	GTG	2811
S	T	T	A	D	G	L	A	Y	Y	D	T	D	E	N	A	P	V	
GCG	TAC	ACA	GAT	GCT	AAC	GGC	GAT	TTG	ATT	TTG	ACG	AAT	GAA	TCA	ATT	TAT	GGT	2865
A	Y	T	D	A	N	G	D	L	I	F	T	N	E	S	I	Y	G	
GTA	CAA	AAT	CCA	CAA	GTT	TCT	GGT	TAC	TTG	GCA	GTT	TGG	GGT	CCG	GTA	GGT	GGG	2919
V	Q	N	P	Q	V	S	G	Y	L	A	V	W	V	P	V	G	A	
CAA	CAA	GAT	CAA	GAT	GCA	CGA	ACG	GCC	TCT	GAT	ACA	ACA	ACA	AAC	ACG	AGT	GAT	2973
Q	Q	D	Q	D	A	R	T	A	S	D	T	T	N	T	S	D		
AAA	GTG	TTC	CAT	TCA	AAC	GCT	GCT	CTT	GAT	TCT	CAA	GTC	ATC	TAC	GAA	GGT	TTC	3027
K	V	F	H	S	N	A	A	L	D	S	Q	V	I	Y	E	G	F	
TCA	AAC	TTC	CAA	GCA	TTT	GCT	ACA	GAC	AGC	AGT	GAA	TAT	ACA	AAC	GTA	GTC	ATC	3081
S	N	F	Q	A	F	A	T	D	S	S	E	Y	T	N	V	V	I	
GCT	CAG	AAT	GCG	GAC	CAA	TTT	AAG	CAA	TGG	GGT	GTG	ACA	AGC	TTC	CAA	TTG	GCA	3135
A	Q	N	A	D	Q	F	K	Q	W	G	V	T	S	F	Q	L	A	
CCA	CAA	TAT	CGT	TCA	AGT	ACA	GAT	ACA	AGT	TTC	TTG	GAT	TCA	ATT	ATT	CAA	AAC	3189
P	Q	Y	R	S	S	T	D	T	S	F	L	D	S	I	I	Q	N	
GGG	TAT	GCA	TTC	ACG	GAT	CGT	TAT	GAC	TTA	GGT	TAT	GGC	ACA	CCG	ACA	AAA	TAT	3243
G	Y	A	F	T	D	R	Y	D	L	G	Y	G	T	P	T	K	Y	
GGA	ACT	GCT	GAT	CAG	TTG	CGC	GAT	GCT	ATT	AAA	GCC	TTA	CAT	GCT	AGC	GGT	ATT	3297
G	T	A	D	Q	L	R	D	A	I	K	A	L	H	A	S	G	I	

FIG.4-4

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CAA	GCC	ATT	GCC	GAT	TGG	GTG	CGC	GAC	CAA	ATT	TAT	AAT	TTG	CCA	GAG	CAA	GAA	3351
Q	A	I	A	D	W	V	P	D	Q	I	Y	N	L	P	E	Q	E	
TTA	GCT	ACT	GTC	ACA	AGA	ACA	AAT	TCA	TTT	GGA	GAT	GAC	GAT	TCT	GAT			3405
L	A	T	V	T	R	T	N	S	F	G	D	D	D	T	D	S	D	
ATT	GAC	AAT	GCC	TTA	TAT	GTT	GTA	CAA	AGT	CGT	GGG	GGT	CAA	TAT	CAA	GAG		3459
I	D	N	A	L	Y	V	V	Q	S	R	G	G	G	Q	Y	Q	E	
ATG	TAT	GGT	GGT	GCC	TTC	TTA	GAA	GAG	TTA	CAG	GCA	CTC	TAT	CCA	TCC	CTA	TTT	3513
M	Y	G	G	A	F	L	E	E	L	Q	A	L	Y	P	S	L	F	
AAA	GTG	AAT	CAA	ATC	TCA	ACT	GGC	GTG	CCA	ATT	GAT	GGC	AGT	GTA	AAG	ATT	ACT	3567
K	V	N	Q	I	S	T	G	V	P	I	D	G	S	V	K	I	T	
GAG	TGG	GCG	GCT	AAG	TAC	TTC	AAT	GGC	TCT	AAC	ATC	CAA	GGT	AAA	GGT	GCT	GGA	3621
E	W	A	A	K	Y	F	N	G	S	N	I	Q	G	K	G	A	G	
TAC	GTA	TTG	AAA	GAT	ATG	GGT	TCT	AAT	AAG	TAC	TTT	AAG	GTC	GTT	TCG	AAC	ACT	3675
Y	V	L	K	D	M	G	S	N	K	Y	F	K	V	V	S	N	T	
GAG	GAT	GGT	GAC	TAC	TTA	CCA	AAA	CAG	TTA	ACT	AAT	GAT	CTG	TCA	GAA	ACT	GGC	3729
E	D	G	D	Y	L	P	K	Q	L	T	N	D	L	S	E	T	G	
TTT	ACA	CAC	GAT	GAT	AAA	GGA	ATC	ATC	TAT	TAT	ACA	TTA	AGT	GGT	TAT	CGT	GCC	3783
F	T	H	D	D	K	G	I	I	Y	Y	T	L	S	G	Y	R	A	
CAA	AAT	GCA	TTT	ATT	CAA	GAT	GAT	AAT	AAC	TAT	TAC	TAT	TTT	GAT	AAA	ACA		3837
Q	N	A	F	I	Q	D	D	N	N	Y	Y	F	.	D	K	T		
GGT	CAT	TTA	GTA	ACA	GGT	TTG	CAA	AAG	ATT	AAT	AAC	CAT	ACC	TAC	TTC	TTC	TTA	3891
G	H	L	V	T	G	L	Q	K	I	N	N	H	T	Y	F	F	L	
CCT	ATT	GGT	ATC	GAA	CTG	GTC	AAG	AGC	TTC	TCA	AAAC	GAA	GAT	GGT	ACA	ATT		3945
P	N	G	I	E	L	V	K	S	F	L	Q	N	E	D	G	T	I	
GTT	TAT	TTC	GAT	AAG	AAA	GGT	CAT	CAA	GTT	TTT	GAT	CAA	TAT	ATA	ACT	GAT		3999
V	Y	F	D	K	K	G	H	Q	V	F	D	Q	Y	I	T	D	Q	
AAT	GGA	AAT	GCG	TAT	TAC	TTT	GAT	GCT	GGT	GTA	ATG	CTT	AAA	TCA	GGG	CTT		4053
N	G	N	A	Y	Y	F	D	A	G	V	M	L	K	S	G	L		
GCA	ACG	ATT	GAT	GGA	CAT	CAA	CAG	TAT	TTT	GAT	CAA	AAT	GGT	GTG	CAG	GT	AAG	4107
A	T	I	D	G	H	Q	Q	Y	F	D	Q	N	G	V	Q	V	K	

FIG.4-5

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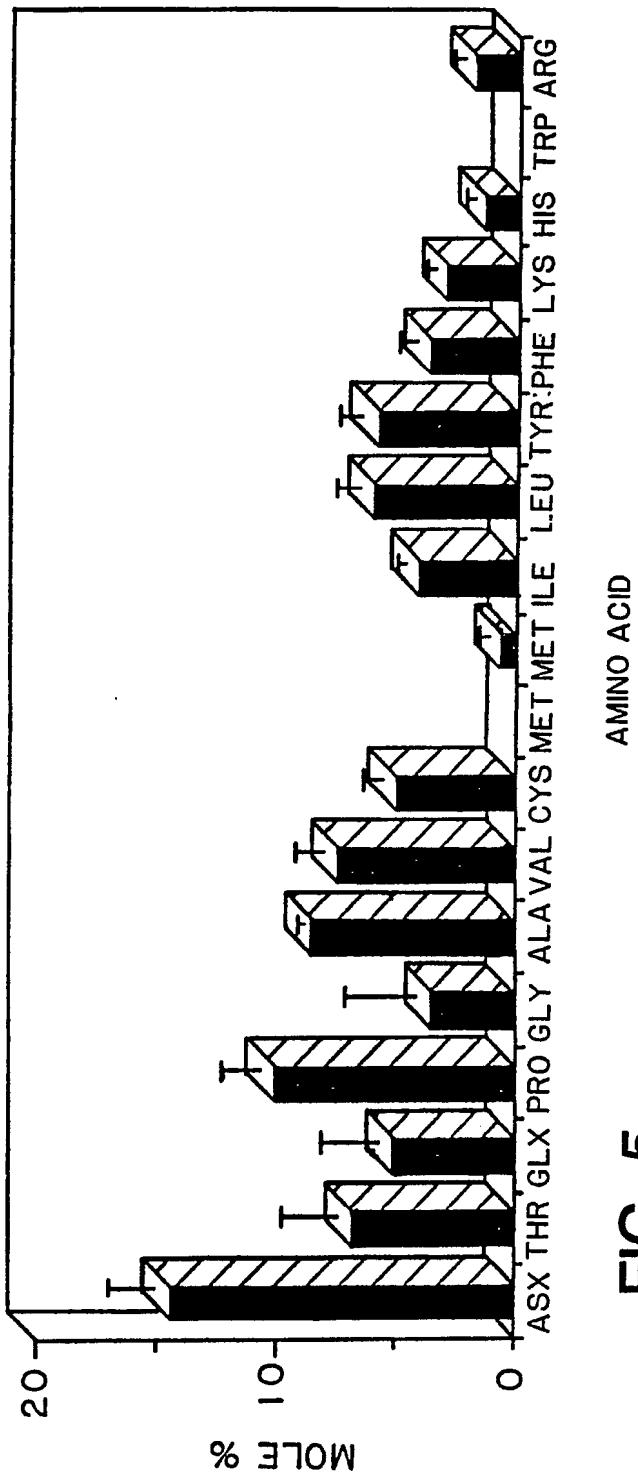
GAT	AAG	TTT	GTG	ATT	GGC	ACT	GAT	GGT	TAT	AAG	TAT	TAC	TTT	GAA	CCA	GGT	AGT	
D	K	F	V	I	G	T	D	G	Y	K	Y	F	E	P	G	S	4161	
GGT	AAC	TTA	GCT	ATC	CTA	CGT	TAT	GTG	CAA	AAT	AGT	AAG	AAT	CAA	TGG	TTC	TAT	
G	N	L	A	I	L	R	Y	V	Q	N	S	K	N	Q	W	F	Y	
TTT	GAT	GGT	AAT	GGC	CAT	GCT	ACT	GGT	TTC	CAA	ACA	ATT	AAT	GGT	AAA	AAA	4215	
F	D	G	N	G	H	A	V	T	G	F	Q	T	I	N	G	K	4269	
CAA	TAT	TTC	TAT	AAT	GAT	GGT	CAT	CAA	AGT	AAA	GGT	GAA	TTC	ATT	GAT	GCA	GAC	
Q	Y	F	Y	N	D	G	H	Q	S	K	G	E	F	I	D	A	4323	
GGG	GAT	ACT	TTC	TAT	ACG	AGT	GCC	ACT	GAT	GGT	CGC	CTA	GTA	ACT	GGT	GTT	CAG	
G	D	T	F	Y	T	S	A	T	D	G	R	L	V	T	G	V	4377	
AAG	ATT	AAT	GGT	ATT	ACC	TAT	GCT	TTT	GAT	AAC	ACA	GGG	AAT	TTG	ATC	ACA	AAT	
K	I	N	G	I	T	Y	A	F	D	N	T	G	N	L	I	T	4431	
CAG	TAT	TAT	CAA	TTA	GCA	GAT	GGT	AAA	TAT	ATG	TTG	TTA	GAT	GAT	AGT	GGT	CGT	
Q	Y	Y	Q	L	A	D	G	K	Y	M	L	L	D	D	S	G	4485	
GCG	AAA	ACA	GGG	TTT	GTA	TTG	CAA	GAT	GGT	GTA	CTA	AGA	TAC	TTC	GAT	CAA	AAC	
A	K	T	G	F	V	L	Q	D	G	V	L	R	Y	F	D	Q	4539	
GGT	GAG	CAA	GTG	AAA	GAT	GCT	ATC	ATT	GTG	GAT	CCA	GAT	ACT	AAC	TTG	AGT	TAT	
G	E	Q	V	K	D	A	I	I	V	D	P	D	T	N	L	S	4593	
TAT	TTC	AAAT	GCA	ACA	CAA	GGT	GTC	GCT	GTA	AAA	AAT	GAT	TAT	TTC	GAG	TAT	CAA	
Y	F	N	A	T	Q	G	V	A	V	K	N	D	Y	F	E	Y	Q	
GGT	AAT	TGG	TAT	TTA	ACA	GAT	GCT	AAT	TAT	CAA	CTT	ATC	AAA	GGT	TTT	AAA	GCA	
G	N	W	Y	L	T	D	A	N	Y	Q	L	I	K	G	F	K	4647	
GTT	GAC	GAC	AGC	TTA	CAA	CAT	TTT	GAT	GAA	GTC	ACT	GGT	GTA	CAA	ACA	AAA	GAT	
V	D	D	S	L	Q	H	F	D	E	V	T	G	V	Q	T	K	4755	
AGT	GCT	TTA	ATA	AGT	GCT	CAG	GGT	AAG	GTT	TAC	CAA	TTT	GAT	AAT	GGA	AAT	4809	
S	A	L	I	S	A	Q	G	K	V	Y	Q	F	D	N	N	G	4875	
GCT	GTG	TCA	GCA	TA	GCT	TCT	GTA	TAT	AGT	GAA	AAAGCCA	GGT	CCT	TTGGCTT	<	4946		
A	V	S	A	END	----->	----->	----->	----->	----->	----->	----->	----->	----->	----->	----->	----->	----->	
TTGATTAAATTGCTTATTGAAATTTCCTGATGATTCGGCTAATTAAATTTCATTCTTTGGCGC																		

FIG. 4-6

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AMINO ACID COMPOSITION - DEXTRANSUCRASE

FIG. 5
AMINO ACID

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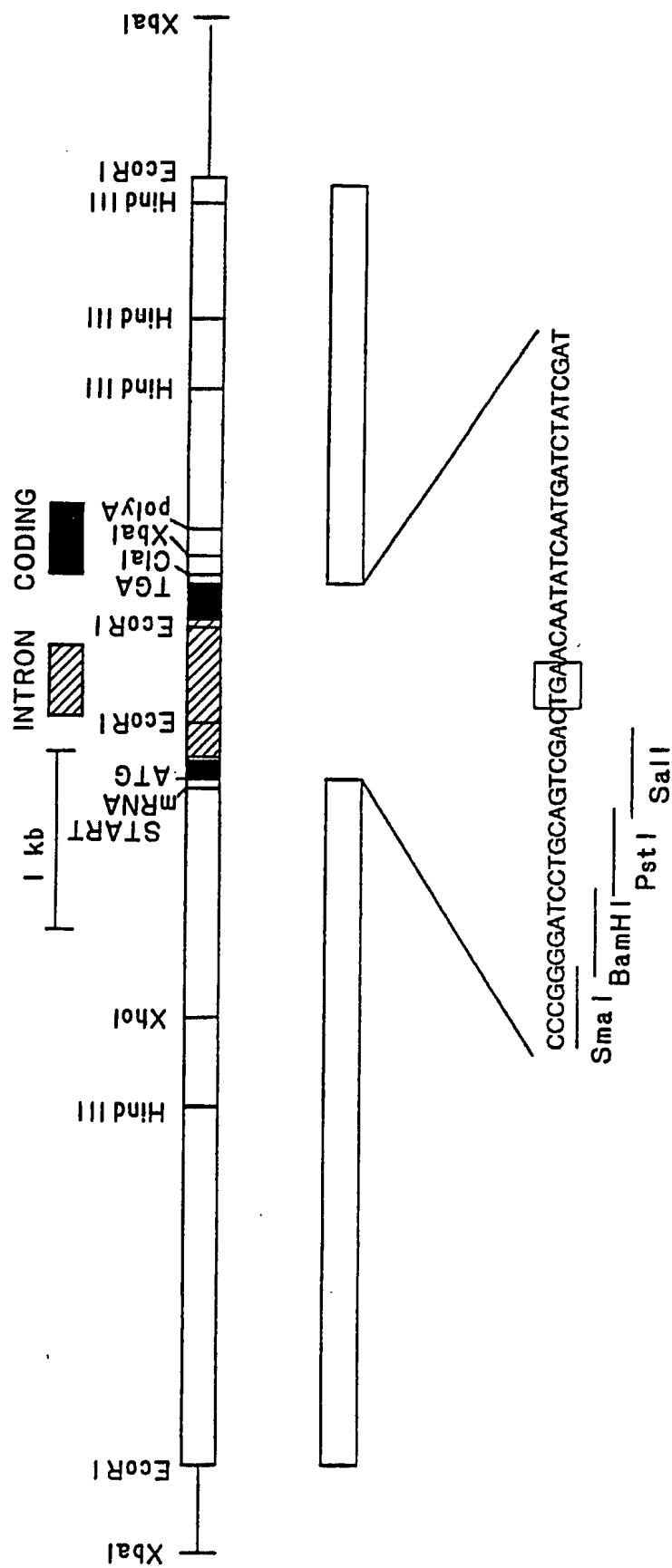


FIG. 6

SUBSTITUTE SHEET

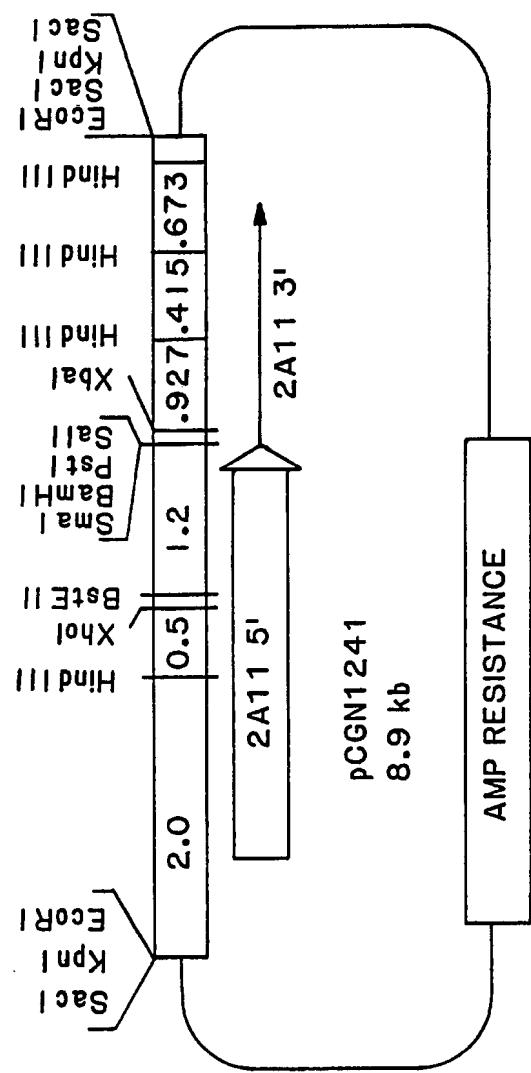


FIG. 7

SUBSTITUTE SHEET

Insert from original dax clone pCGN1222:

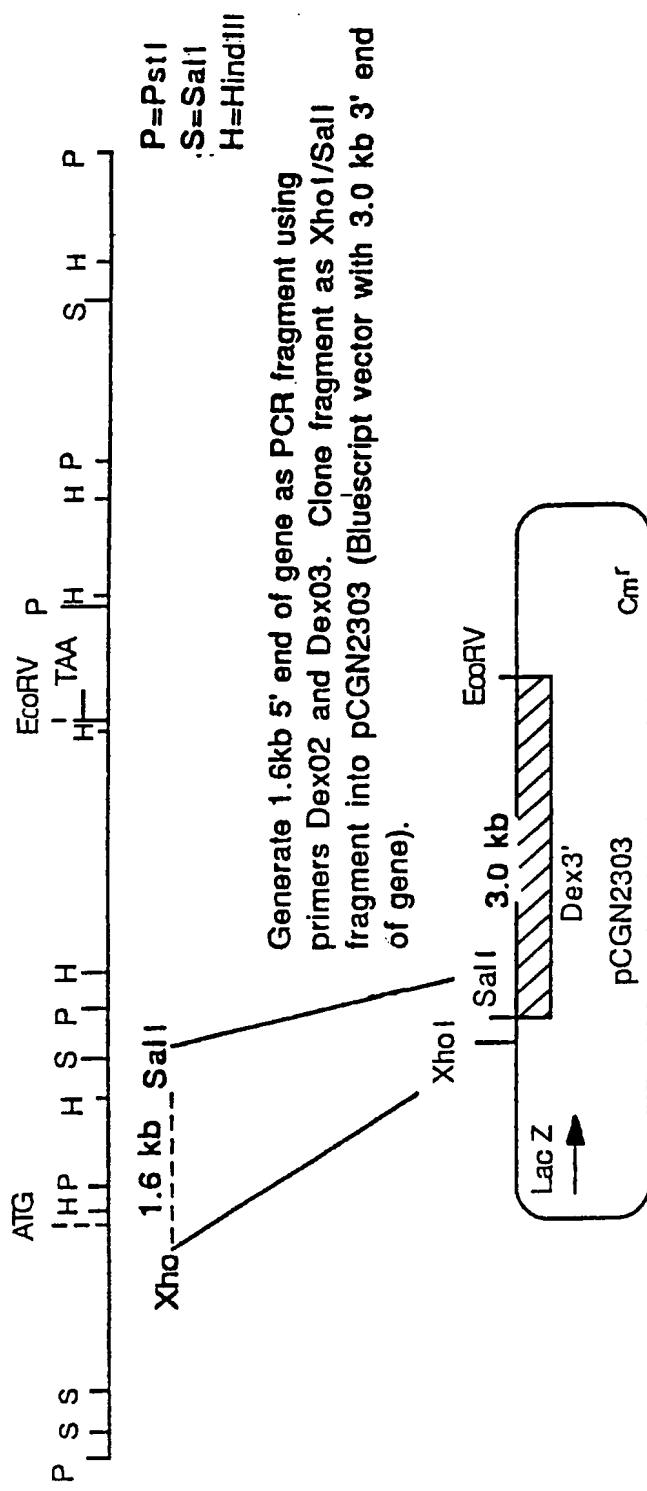
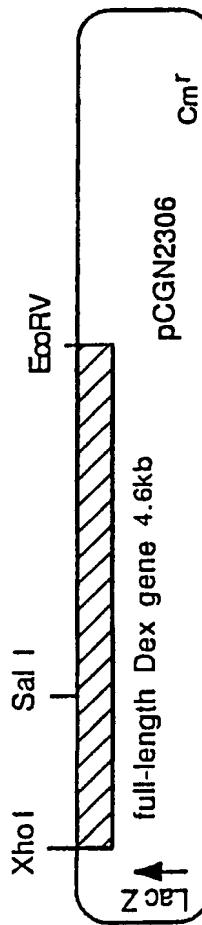
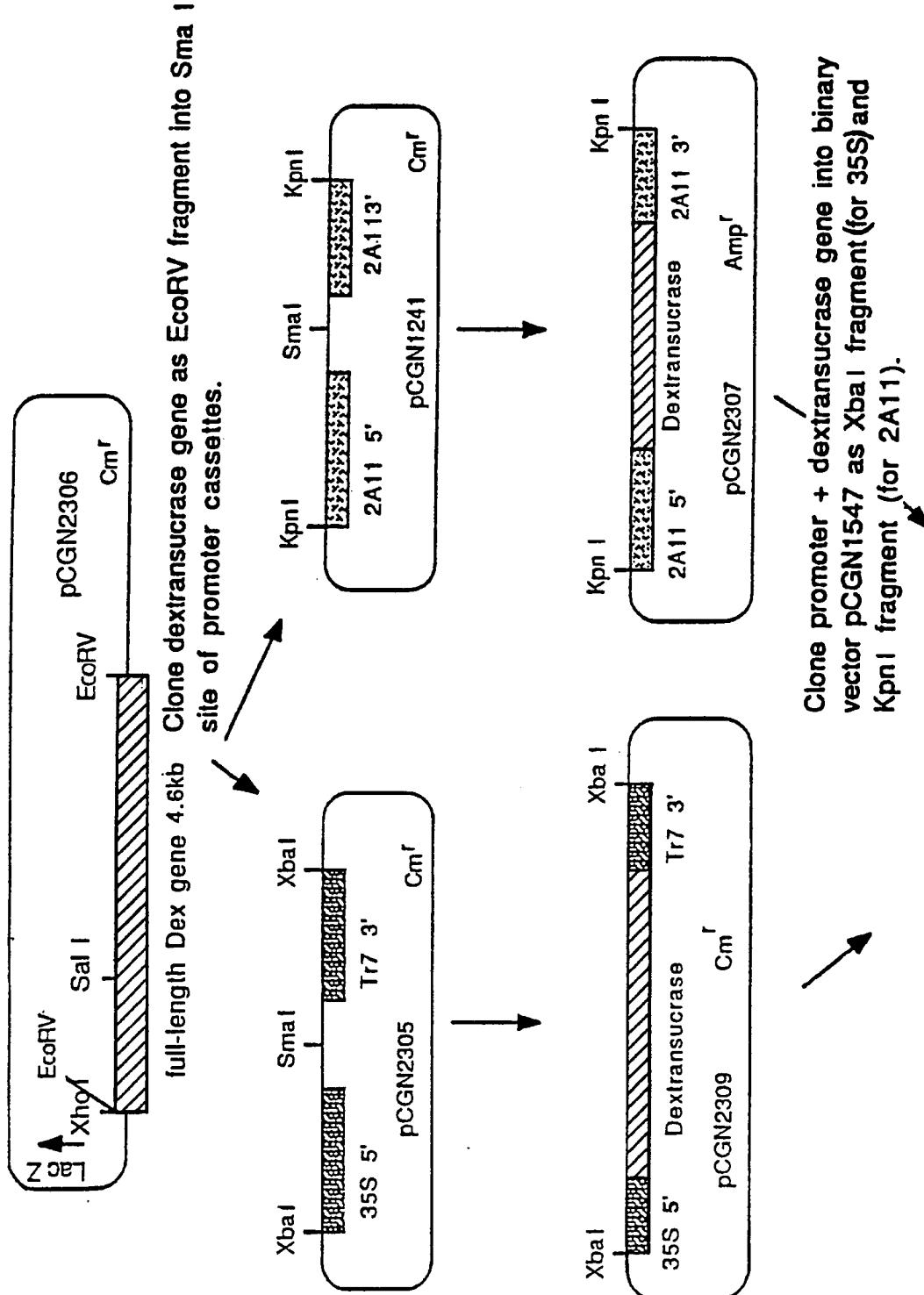


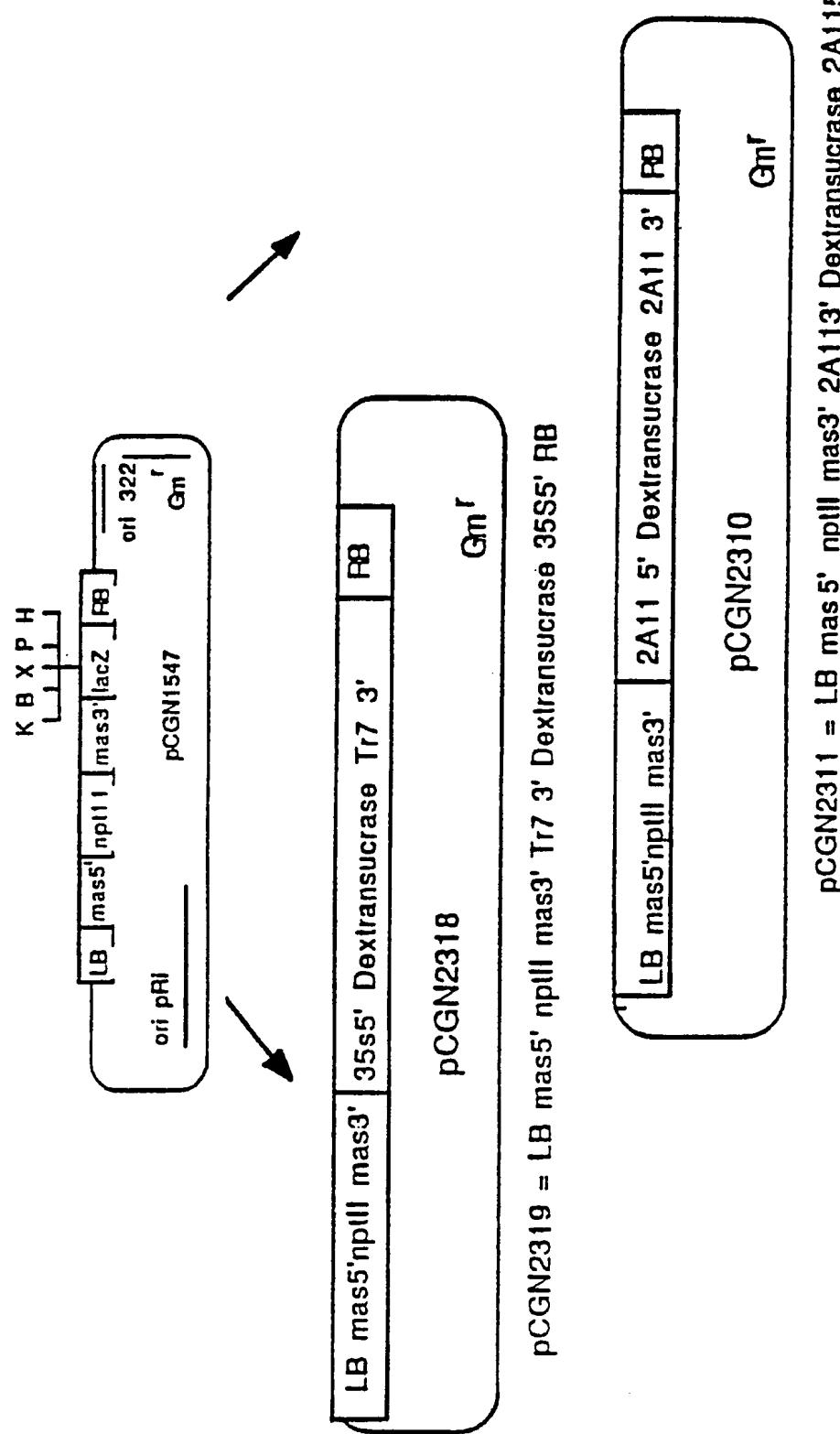
FIG. 8



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FIG. 9 - 1**SUBSTITUTE SHEET**

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**FIG. 9-2**

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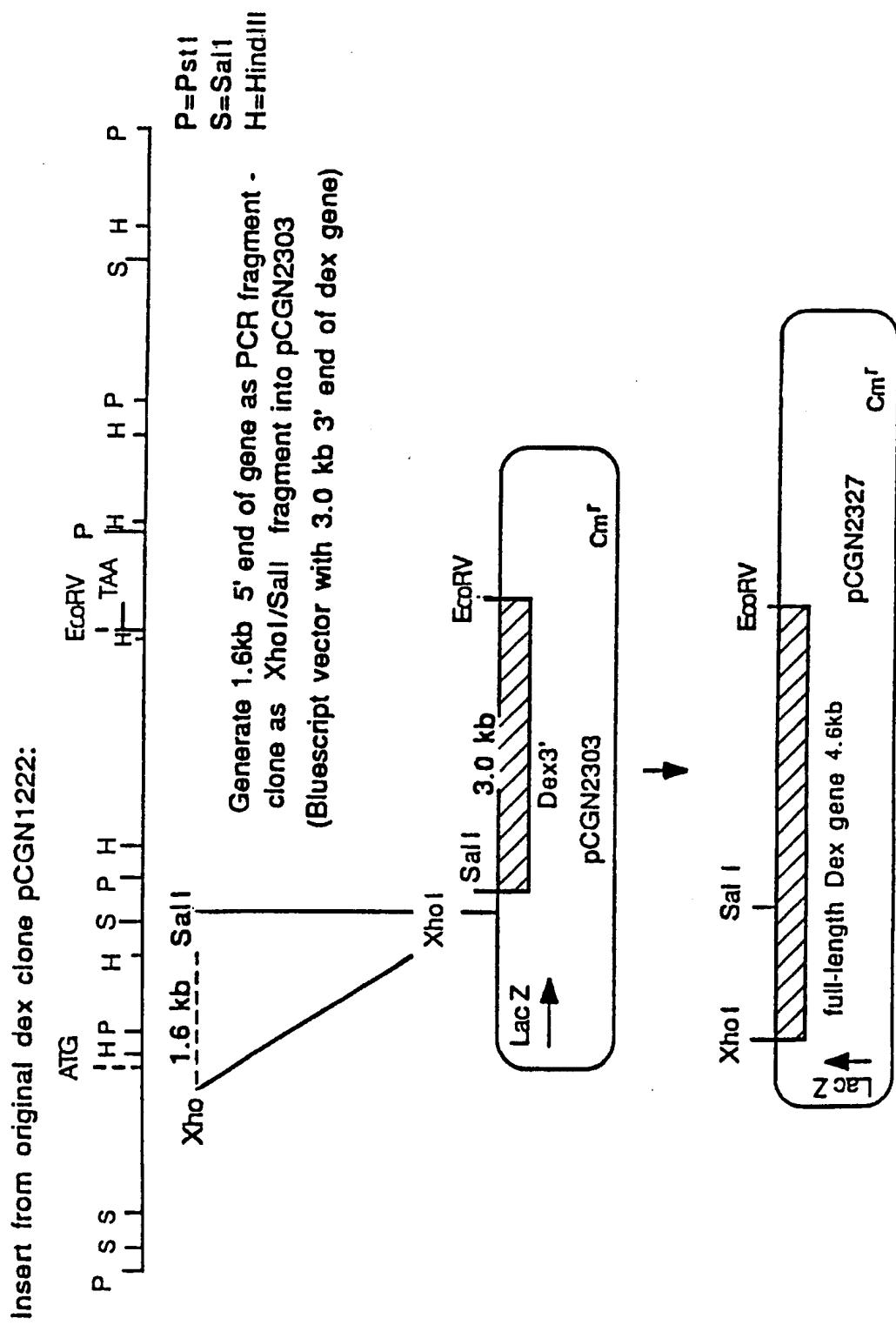
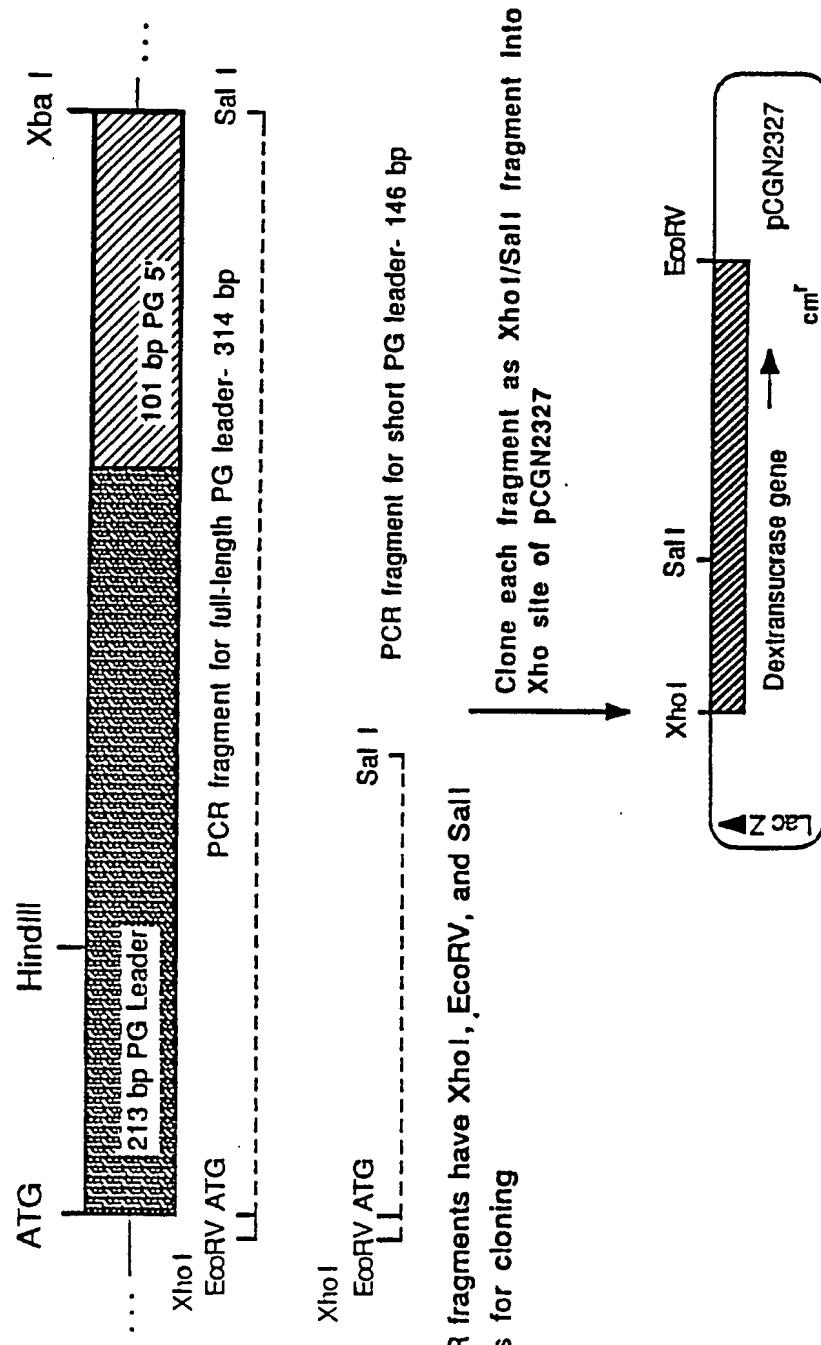


FIG. 10

PG leader and 5' region from pCGN1407:

FIG. 11-1



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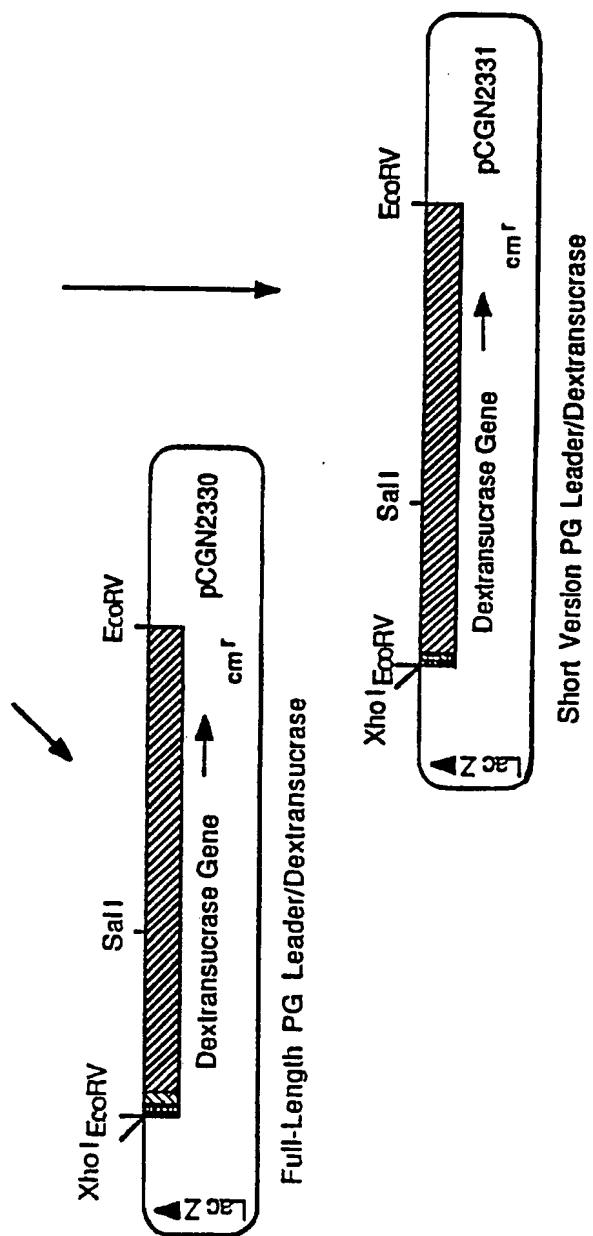


FIG. 11-2

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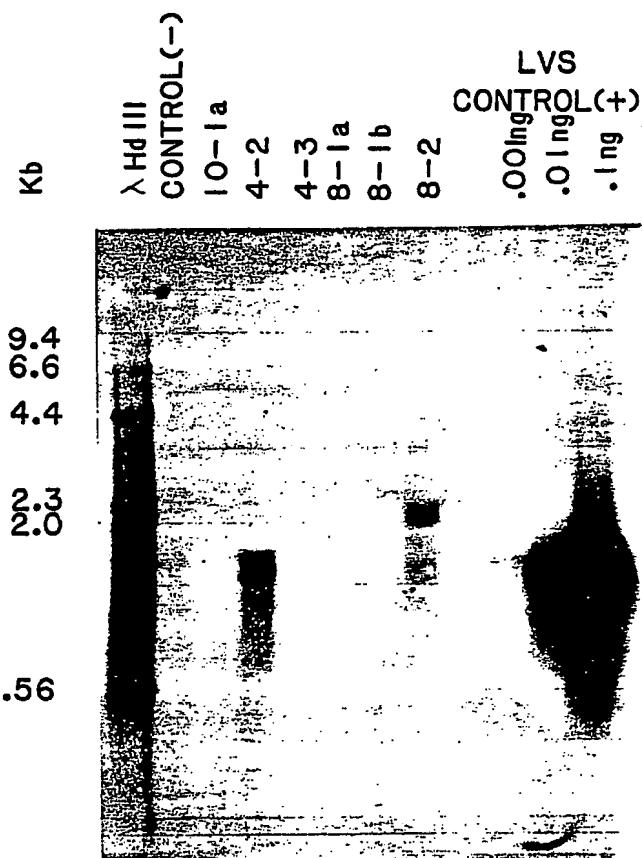


FIG. 12A

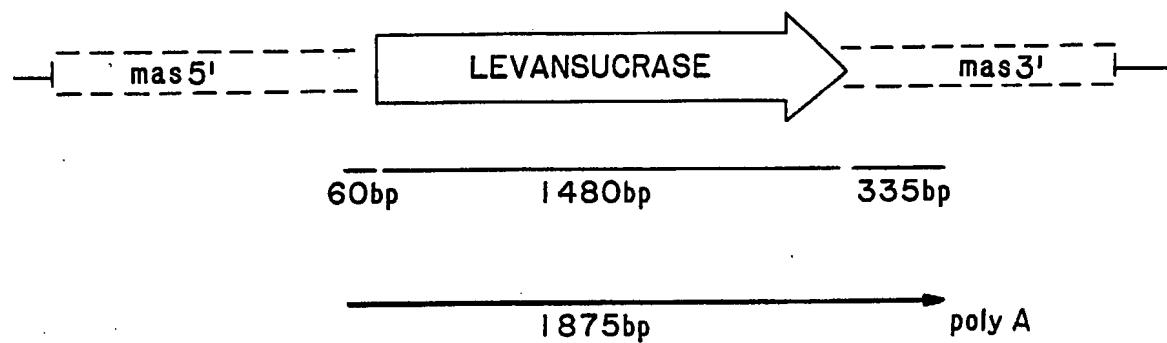


FIG. 12B

SUBSTITUTE SHEET

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US89/02729

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ⁶

According to International Patent Classification (IPC) or to both National Classification and IPC

**IPC(4): A01H 1/04; C12N 1/00; C12N 5/00; C12N 15/00; C07H 21/04
U.S.CL.: 800/1; 435/172.1, 172.3, 240.4, 317.1, 320; 536/27**

II. FIELDS SEARCHED

Minimum Documentation Searched ⁷

Classification System	Classification Symbols
U.S.	536/27 435/172.1, 172.3, 240.4, 317.1, 320 800/1

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched ⁸

USPTO Automated Patent System; DIALOG files: BIOTECH,
PATENTS, WORLD PATENTS INDEX, See Attachment for search terms.

III. DOCUMENTS CONSIDERED TO BE RELEVANT ⁹

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
P,X,Y	US, A, 4,801,540 (HIATT) 31 January 1989, See entire document and page 4, lines 65-68.	1-30
A	Hortscience (St. Joseph, Michigan USA), Volume 13, Issued December 1978, Stevens et al, "Genetic potential for overcoming physiological limitations an adaptability, yield, and quality in the tomato", pages 673-678.	1-30
Y	Journal of Bacteriology (Washington DC, USA) Volume 153, Issued 1983, Gay et al., "Cloning structural Gene sacB, which codes for exenzyme levansucrase of Bacillus subtilis: Expression of the gene in E. coli", pages 1424-1431.	1-30

* Special categories of cited documents: ¹⁰

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"d" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

7 September 1989

Date of Mailing of this International Search Report

30 OCT 1989

International Searching Authority

ISA/US

Signature of Authorized Officer

P. Rhodes

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET

A	Theoretical and Applied Genetics (New York, USA) Volume 73, Issued 1987, Osborn et al, "Identification of restriction fragment length polymorphisms linked to genes controlling soluble solids content in tomato fruit", pages 350-356.	1-30
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V. OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE¹

This international search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:

1. Claim numbers _____, because they relate to subject matter^{1,2} not required to be searched by this Authority, namely:

2. Claim numbers _____, because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out^{1,2}, specifically:

3. Claim numbers _____, because they are dependent claims not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

VI. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING²

This International Searching Authority found multiple inventions in this international application as follows:

SEE ATTACHMENT.

1. As all required additional search fees were timely paid by the applicant, this International search report covers all searchable claims of the international application.

2. As only some of the required additional search fees were timely paid by the applicant, this International search report covers only those claims of the international application for which fees were paid, specifically claims:

3. No required additional search fees were timely paid by the applicant. Consequently, this International search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:

Telephone Practice

4. As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remark on Protest

The additional search fees were accompanied by applicant's protest.

No protest accompanied the payment of additional search fees.